

SEQUENCE LISTING

SEQ ID NO: 1 human IPM 150 cDNA, isoform A (3330 bp)

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1 TAAACCAAGA AGGTTATCCT CAATCATCTG GTATCAATAT ATAATTATTT TTCACATTTT
61 TGTATCTTTT TAATGAGATT TGAGTTGTTT CTGTGATTGT TATCAGAATT ACCAATGTCAC
121 AAAAGCCAGA ATGTATTGGA AACTAGAAAG AGCTATTTTT GTTTTTTGGT TTTTCTCTCA
181 AGTTCAAGGA ACCAAAGATA TCTCCATTAA CATATACCAT TCTGAAACTA AAGACATAGA
241 CAATCCCCCA AGAAATGAAA CAACTGAAAG TACTGAAAAA ATGTACAAAA TGTCACATAT
301 GAGACGAATA TTCGATTGAG CAAAGCATCG AACAAAAAGA TCCGCATTTT TCCCAACGGG
361 GGTAAAGATG TGTTCCACAGG AATCCATGAA ACAGATTTTA GACAGTCTTT AAGCTTATTA
421 TAGATTGAGA GTGTGTCCAGG AAGCAGTATG GGAAGCATAT CGGATCTTTC TGGATCGCAT
481 CCCTGACACA GGGGAATATC AGGACTGGGT CAGCATCTGC CAGCAGGAGA CCTCTTGCTC
541 CTTTGACATT GGAAAAAAAT TCAGCAATTC CCAGGAGCAC CTGGATCTTC TCCAGCAGAG
601 AATAAAACAG AGAAGTTTCC CTGACAGAAA AGATGAAATA TCTGCAGAGA AGACATTGGG
661 AGAGCCTGGT GAAACCAATT TCATTTCAAC AGCAATCTAC ATTTCAAAGA CTGGGCAGT
721 ATTCTAAGAA AACCCTCAGA AGAGCAAAAT CAAGATGTGG CCAACGCTCT ACTTGGGCTC
781 TTCCCTCTCA CTCTGTATGA CACCCTCCTC AATGAAATTC TCGATAATAC ACTCAACGAC
841 AACAGAGATG CTACAACAGA AAGAGAAACA GAATTCGCTG TGTTGGAGGA GCAGAGGGTG
901 GAGCTCAGCG TCTCTCTGGT AAACCAAGAAG TTCAAGGCGAG AGCTCGCTGA CTCCCAGTCC
961 CCATATTACC AGGAGCTAGC AGGAAAGTCC CAACTTCAGA TGCAAAAAGT ATTTAAGAAA
1021 CTCCAGGAT TCAAAAAAT CCATGTGTGA GGAATTAGAC CAAAGAAAGA AAAAGATGGC
1081 TCAAGCTCCA CAGAGATGCA ACTTACGCCC ATCTTTAAGA GACACAGTGC ACAGAGCAAA
1141 AGCCCTGCAA GTGACCTCCT GTCTTTTGAT TCCAAACAAA TTGAAAGTGA GGAAGTCTAT
1201 CATGGGAACA TGGGAGGAGA CAAGCAACCA GAAATCTATC TCACAGCTAC AGACTCTCAA
1261 AGGCTGATCA GCAAAGCACT AGAGGAAGAA CAATCTTTGG ATGTGGGGAC AATTCAGTTT
1321 ACTGATGAAA TTGCTGGATC ACTGCCAGCC TTTGGTCTCG ACACCCAATC AGAGCTGCCC
1381 ACATCTTTTG CTGTATATAA AGAGGATGCT ACTTTGAGTC CAGAACTTCC TCCTGTTGAA
1441 CCCCAGCTTG AGACAGTGGA CGGAGCAGAG CATGGTCTAC CTGACACTTC TTGGTCTCCA
1501 CCTGCTATGG CCTCTACCTC CTTGTCAAGG GCTCCACCTT TCTTTATGGC ATCAAGCATC
1561 TTCTCTCTGA CTGATCAAGG CACCACAGAT ACAATGGCCA GTGACCAGAC AATGCTAGTA
1621 CCAGGGCTCA CCATCCCCAC CAGTGATTAT TCTGCAATCA GCCAACTGTC TCTGGGAATT
1681 TCACATCCAC CTGCATCTTC AGATGACAGC CGATCAAGTG CAGGTGGCGA AGATATGGTC
1741 AGACACCTAG ATGAAATGGA TCTGTCTGAC ACTCTCGCCC CATCTGAGGT ACCAGAGCTC
1801 AGCGAATATG TTTTGTGCCC AGATCATTTC TTGGAGGATA CCACTCTGCT CTACGCTTTA
1861 CAGTATATCA CCACTAGTTC TATGACCATT GCCCCCAAGG CCAGGAGGCT GTGATGTTCT
1921 TTGAGTCTGC GTGTGCTTAA CATGGCCTTC TCCAACGACC TTGTTCAACAA GAGCTCTCTG
1981 GAGTACCCAG CTCTGGAGCA ACAAATCACA CAGCTGTCTG TCCATATCTC ACGATCCAAT
2041 CTTACAGGAT TTAAGCAACT TGAATACTTT AACTTCAGAA ACGGGAGTGT GATTGTGAAT
2101 AGCAAAATGA AGTTTGTCTA GTCTGTGCCG TATAACCTCA CCAAGCTGTG GCACGGGGTC
2161 TTGGAGGATT TTGCTTCTGC TGCAGCCCAA CAACTCCATC TGGAAATAGA CAGCTACTCT
2221 CTCAACATTT AACCACTGTA TCAAGCAGAT CCCTGCAAGT TCCTGGCCTG CGGCAAGATT
2281 GCCCAATGTG TAAAGAACGA ACGGACTGAG GAAGCGGAGT GTGCTGCAA ACCAGGATAT
2341 GACGCCAGG GAGGCTGGAA CGGTCTGGAA CCAGGCTCTT GTGGCCCTGG CACAAAGGAA
2401 TGCAGGTCCT TCCAGGGAAA GGGAGCTCCA TGCAGTTTGC TGAAGATCAA TGAAGATCAA
2461 GCATACAAAA CTAGTGTTAA AAGTTCCAAA AATCAACAAA ATACAAGGT AATCAGTAAA
2521 AGAAATTTCT GATTTACTGAC CGTAGAATAT GAAGAAATTA ACCATCAAGT TTGGGAGAGA
2581 AATTAATAAAC TGAAATGTGA CAATTATCAC TTAGGCTATC TCAAGAGAGA TGATTTGCTC
2641 TCTCAAGGAA AATGGAGACA GGCATATTCA TGGGTCATCA AATTCAGAG ATACAGTCAA
2701 CACTGAGAAT CAGCACACAC CATATTTCAA ATATAGAAGA GTCATGTACT TGCAACCAAG
2761 TAAATTTCTGA AAAAAAAGAC ACTTACTTAT TATTAAGAAC CCAATGCAAA TCAGCGAAAC
2821 ATATTTTTTAC TATTCTTGGA TGATAGTCAA AATGATCATA AGCCAGGTTT GCTTCCACCT
2881 TCCCTGAAAA TTTTACTCAC AGATCATTTG CACAAGCAT AGCTTACTTA TTGTTTAGGG

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2941	ACTGAACAA	TATTGGGAA	GCAAACTCT	TATATGCTAG	AAAGTACATT	TAAAGATGA
3001	CTACTTACG	AGGGAGATG	AGGTCTCTCT	AAACGCATGA	ATGTATGTAG	TGTGTAGGCA
3061	CTGTAGTGAG	TGTATATATG	CTCCACACTA	CGTCTGTATA	ACACAAACCT	CAGTATTACG
3121	TTATTAGGCA	CACCTAGTTT	ATACGCAACT	ACTGCTTACA	TAGTAGACTC	TTTTGTGGCC
3181	AATAACTCTT	GAATTGTTCT	TAAAGAGAAA	CTGAGGTTCA	GATACACATA	CCATGTAAAA
3241	ATCTTACTTT	TCTTGTTACT	ACACAAGACT	ATTTTAAAGA	AGATGCTATG	TTGGGAGAA
3301	GGCGAAGTTG	TACTATATGA	CATAATCAAT			

SEQ ID NO: 2 Human IPM 150 amino acid sequence, isoform A

1	MYLETRRAIF	VWFIFLQVQG	TKDISINIIH	SETKDIDNPP	RNETTESTEK	MYKMSTMRI
61	FDLAKHRTKR	SAFFPTGVKV	CPQESMKQIL	DSLQAYYRLR	VQCEAVWEAY	RIFLDRIPT
121	GEYQDWISIC	QGETFCLFDI	GKNFNSQEH	LDLLQQRIRK	RSFPDRKDEI	SAEKTLPGE
181	ETIVISTDVA	NVSLGPFPLT	PDDTLNLEIL	DNTLNDTKMP	TERETEFAY	LEEQRVELSV
241	SLVNVQKFAE	LADSQSPYYQ	ELAGKSQMQ	QKIFKKLPGF	KKIHLVGFPR	KKEKDGSSST
301	EMQLTATFKR	HSAEAKSPAS	DLLSFDNSKI	ESEEVYHGT	EEDKQPIYL	TATDLKRLIS
361	KALEEEQSLD	VGTIQFTDEI	AGSLPAFGPD	TQSELPSTFA	VITEDATLSL	ELPVEPQLE
421	TVDGAEHGLP	DTWSPPAMA	STSLSEAPPF	FMASSIFSLT	DQGTDTMTAT	DQTHLVPLGT
481	IPTSDFSAIS	QLALGISHP	ASSDDSRSSA	GGEDHVRHLD	EMDLSDTTAP	SEVPELSEYV
541	VPDHFLEDT	TPVSALQYIT	TSSMTIAPKG	RELVVFFSLR	VANMAFSNDL	FNKSLELYRA
601	LEQQFTQLLV	PYLRNSLTGF	KQLEILNFRN	GSVIVNSMKM	FAKSVPPNLT	KAVHGVLEDF
661	RSAAAGQLHL	EIDSYSLNIE	PADQADPKCF	LACGEFAECV	KNERTEAEAC	RCKPGYDSQG
721	SLDGLPEPLC	GPGTKECEVL	QKGGAFCRLP	DHSENNQAYK	SVKKFQNNQN	NKVISKRNSE
781	LLTVEYEEFN	HQDWEGN				

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SEQ ID NO: 3 Human IPM 150 cDNA sequence, isoform B

1	GGGAGCTATT	TTTGTTTTTT	GGATTTTCT	CCAAGTTCAC	GGAACCAAG	TGTGTCAGGA
61	AGCAGTATGG	GAAGCATATC	GGATCTTTCT	GGATCGCATC	CCTGACACAG	GGGAATATCA
121	GGACTGGGTC	AGCATCTGCC	AGCAGGAGAC	CTTCTGCCTC	TTTGACATTG	GAAAAAATCT
181	CAGCAATTC	CAGGAGCACC	TGGATCTTCT	CCAGCAGAGA	ATAAAACAGA	GAACTTTCCC
241	TGACAGAAAA	GATGAAATAT	CTGCAGAGAA	GACATTGGGA	CTGCAAGTG	AAACCAATTGT
301	CATTTCACCA	GATGTTGCCA	ACGTCTCACT	TGGGCTTTCT	CTCTCACTAC	CTGATGACAC
361	CCTCTCAAT	GAAATCTCG	ATAATACACT	CAACGACACC	AAGATGCCCTA	CAACAGAAAG
421	AGAAACAGAA	TTCGCTGTGT	TGGAGGAGCA	GAGGTGGGAG	CTCAGCGTCT	CTCTGGTAAA
481	CCAGAAGTTC	AAGGCAGAGC	TCGCTGACTC	CCAGTCCCCA	TATTACCAGC	AGCTAGCAGG
541	CAAGATCCCA	CTTCAGATGC	AAAAGATATG	TAAGAAACTT	CAGGATTCCA	AAAAAATCCA
601	TGTTGTTAGGA	TTTAGACCAA	AGAAAGAAAA	AGATGGCTCA	AGCTCCACAG	AGATGCACAT
661	TACGGCCATC	TTTAAGAGAC	ACAGTGCAGA	AGCAAAAAGC	CTCTGCAAGT	ACCTCTTGTC
721	TTTGTATTCC	AACAAAAATTG	AAAGTGAGGA	AGTCTATCAT	GGAACCATGG	AGGAGGACAA
781	GCAACAGAGAA	ATCTATCTCA	CAGCTACAGA	CCTCAAAAGG	CTGATCAGCA	AAGCACTAGA
841	GGAAGAACAA	TCITTTGGATG	TGGGGACAAT	TCAGTTCACT	GATGAAATTG	CTGGATCACT
901	GCGACGCTTT	GGTCCCTGACA	CCCAATCAGA	GCTGCCACAC	CTTTTGTGCT	TTATACAGAA
961	GGATGCTACT	TTGAGTCCAG	AACTTCTTCC	TGTGAAACCC	CAGCTTGAGA	CAGTGGACGG
1021	AGCAGACAT	GGTCTACCTG	ACACTTCTTG	GTCTGCGCTT	CTGATGCTCT	TACTCTCTCT
1081	GTCAGAAGCT	CCACCTTTCT	TTATGGCATC	AAGCATCTTC	TCTCTGACTG	ATCAAGGCAC
1141	CAGACATACA	ATGGCCACTG	ACCAGACAAT	GCTAGTACCA	GGGCTCACCA	TCCCCACAG
1201	TGATTATCTT	GCAATCAGCC	AACTGGCTCT	GGGAATTTCA	CATCCACTCT	CATCTTCAGA
1261	TGACAGCCGA	TCAAGTGCAG	GTGGCGAAGA	TATGGTCAGA	CACTAGATGT	AAATGGATCT
1321	GTCTGACACT	CCGTGCCCAT	CTGAGGTACC	AGGGCTCAGC	GAGTCTGGTG	CTGTCCCGAG
1381	TACATTTCTTG	GAGGATACCA	CTCCTGTCTC	AGCTTTACAG	TATATCACCA	CTAGTTCTAT
1441	GCACTATTGCC	CCCAAGGGCC	GAGAGCTGGT	AGTGTCTTCT	AGTCTGGGTC	TTGTAAACAT
1501	GGCCTTCTCC	ACAGCCTGTG	TCAACAAGAG	CTCTCTGGAG	TACCGAGCTC	TGGAGCAACA
1561	ATTACACACG	CTGCTGGTTC	CATATCTACG	ATCCAACTCT	ACAGGATTTA	AGCAAGTTGA
1621	AATACTTAAC	TTCAGAAACG	GGAGTGTGAT	TGTGAATAGC	AAAATGAAGT	TTGCTAAGTC

1681	TGTGCGGTAT	AACCTCACCA	AGGCTGTGCA	CGGGGTCTTG	GAGGATTTTC	GTTCTGCTGC
1741	AGCCCAACAA	CTCCATCTGG	AAATAGACAG	CTACTCTCTC	AACATTGAAAC	CAGCTGATCA
1801	AGCAGATCCC	TGCAAGTTCC	TGGCCTGCGG	CGAATTTGCC	CAATGTGTAA	AGAACGAACG
1861	GACTGAGGAA	GCGGAGTGTG	GCTGCAAAAC	AGGATATGAC	AGCCAGGGGA	GCCTGGACCG
1921	TCTGGAAACA	GGCCTCTGTG	GCCCTGGCAC	AAAGGAATGC	GAGGTCTCTC	AGGGAAAGGG
1981	AGCTCCATGC	AGGTTGCCAG	ATCACTCTGA	AAATCAAGCA	TACAAAACTA	GTGTTAAAAA
2041	GTTCCAAAAA	CAACAAAAAT	ACAAGGTAAT	CAGTAAAGA	AATTCGTAAT	TACTGACCGT
2101	AGAATATGAA	GAATTTAAAC	ATCAAGATTG	GGAAGGAAAT	TAAAAACTGA	AAATGTACAA
2161	TTATCACTTA	GGCTATCTCA	AGAGAGATGA	TTTGCTTTCT	CAAGGAAAAA	GGAGACAGCG
2221	ATATTCTATG	GCTCATAAAA	TCCAGACATA	CAGTCAACAC	TGGAAATCAG	CACACACCAT
2281	ATTTCAAAAT	TAGAAGAGTC	ATGTACTTGG	CAACCAGTAA	ATTCGTAAAA	AAAAGACACT
2341	TACTTATTAT	TAAACCCCA	AATGCAATCA	GCGAAACATA	TTTTTACTAT	TCTTGGATAG
2401	TAGTCAAAAT	GATCATAAGC	CAGGTTTGCT	TCCACCTTCC	CTGAAAAATT	TACTCACAGA
2461	TCATTTTGCA	CAAGCATAGC	TTACTTTATT	TTTAGGGACT	GAACAATTTA	TGGGAAGACA
2521	AACCTCTTAT	ATCATAGAAA	GTACATTTAA	AAGATGACTA	CTTAGCGAGG	GAGATGCGAG
2581	TCTCTCTAAA	GCGTGAATGT	TATGTAGTGT	TAGGGCACTG	GTAGGCACTG	ATATATGCTC
2641	CACACTACGT	CTGATAAACA	CAAACTCTAG	TATTCAGTTA	TTAGGCACAC	TAGTTTTATA
2701	CGCAACTACT	GTTTACATAG	TAGACTGTTT	TGTTGCCAAT	AATCTTTGAA	TTGTTCTTTA
2761	AAAGAACTGT	AGGTTGAGAT	ACACATACCA	TGGAATAATC	TTACTTTTCT	TGTTACTACA
2821	CAAAGCTATT	TTAAAGAAGA	TGCTATGTTG	GGAGAAAGGC	GAAGTGTGAT	TATATGACAT
2881	AATCAAT					

SEQ ID NO: 4 Human IPM 150 amino acid sequence, isoform B

1	MYLETRRAIF	VFWIFLQVQG	TKVCQEAVWE	AYRIFLDRIP	DTGEYQDWVS	ICQQETFCFL
61	DIGKNFSNQS	EHLDDLQQR	KQRSFPDRKD	EISAEKTLGE	PGETIVISTD	VANVSLGPFP
121	LTPDLDLLNE	LTPDLDLLNE	MPTTERETEF	AVLEENQKFK	SVSLVNGQFK	AEALDSQSPY
181	YQELAGKSQL	QMQKIFKKLP	GFKKIHLVGF	RPKKEKDGSS	STEMQLTATF	KRHSAEAKSP
241	ASDLLSFDNS	KIESEEVYHG	TMEEDKQPEI	YLATDCLKRL	ISKALEEEQS	LDVGTIQFTD
301	EIAGSLPAFG	PDTQSELPIS	FAVITEDATL	SPELPPVEPQ	LETVDGAHEG	LPDTSWSPPA
361	MASTSLSEAP	PFFMASSIFS	LTDQGTDTDM	ATDQTMVLPV	LTIPTSDYSA	ISQLALGISH
421	PPASSDDRS	SAGGEDMVRH	LDEMDSLSTP	APSEVPLGLE	YVSVDPHFLE	DTTPVSALQY
481	ITTSMTIAP	KGRELVVFFS	LRVANMAFSN	DLFNKSSLEY	RALEQQFTQL	LVPLYRSNLT
541	GFKQLEILNF	RNGSVIVNSK	MKFAKSVVPN	LTKAVHGVLE	DFRSAQAQQL	HLEIDSYSLN
601	IEPADQADPC	KFLACGEFAQ	CVKNERTEEA	ECRCRPGYDS	QGSLDGLEPG	LCGPGTKECE
661	VLQKGAPCR	LPDHSNQAY	KTSVKKFQNG	QNNKVISKRN	SELLTVEYEE	FNHQDWEGN

SEQ ID NO: 5 Human IPM 150 cDNA sequence, isoform C

1	AAATTAACAC	CCTCATAAAG	GTAACCAAG	AAGGTTATCC	TCAATCATCT	GGTATCAATA
61	TATAATTATT	TTTCACATTT	CTGTTACTTT	TTAATGAGAT	TTGAGGTTGT	CTGTGATTTG
121	TATCAGAATT	ACCAATGCAC	AAAAGCCAGA	ATGTAATTTG	AACTVAGAKF	AGCTATTTTT
181	GTITTTTTGA	TTTTTCTCCA	AGTTCAAGGA	ACCAAAGATA	TCTCCATTAA	CATATACCAT
241	CTGAAACTA	AAGACATAGA	CAATNCCCCA	AGAAATGAAA	CAACTGAAAG	TACTGAAAAA
301	ATGTACAAAA	TGTCAACTAT	GAGACGAATA	TTCGATTTGG	CAAGNATCG	AACAAAAAGA
361	TCCGCATTTT	TCCCAACGGG	GGTTAAAGTC	TGTCACAGG	AATCCATGAA	ACAGATTTTT
421	GACAGCTCTT	AACTCTTATTA	TAGATTGAGA	GTGTGTGAGG	AGGACGATG	GGAAGCATAT
481	CGGATCTCTT	TGGATCGCAT	CCCTGACACA	GGGGAATATC	AGGACTGGGT	CAGCATCTGC
541	CAGACGAGCA	CCTTCTGCCT	CTTTGACATT	GGAAAAAAGC	TCAGCAATTG	CAGCAGACAC
601	CTGGATCTCT	TCCAGCAGAG	AATAAAACAG	AGAAAGTTCC	CTGACGAAAA	AGATGAAATA
661	TCTGCAGAGA	AGACATTGGG	AGAGCCTGGT	GAAACCATTG	CTATTTCAAC	AGCAATCTAC
721	ATTTCAAAGA	CTTTGGGCAGT	ATTCTAAGAA	AACCTCTAGA	AGAGCAAACT	CAAGATGTTG
781	CCACGTCCTC	ATTTGGGCTC	TTCCCTCTCA	CTCCTGATGA	CAACCTCTC	AATGGAATTC
841	TCGATAATAC	ACTCAACGAC	ACCAAGATGC	CTACAACAGA	AAGAGAAACA	GAATTGCGTG
901	TGTTGGAGGA	GCAGAGGGTG	GAGCTCAGCG	TCTCTCTGGT	AAACCAGAAG	TTCAGGCAG

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961 AGCTCGTGTA CTCCCAGTCC CCATATTACC AGGAGCTAGC AGGAAAGTCC CAACTTCAGA
1021 TGCAAAAGAT ATTTAAGAAA CTTCAGGAT TCACAAAAT CAGTGTGTTA GGATTTAGAC
1081 CAAAGAAAGA AAAAGATGGC TCAAGCTCCA CAGAGATGCA ACTTACGGCC ATCTTTAAGA
1141 GACACAGTGC AGAAGCAAAA AGCCCTGC AA GTGACCTCCT GTCTTTTGAT TCCAACAAAA
1201 TTGAAAGTGA GGAAGCTAT CATGGAAACA TGGAGGAGGA CAAAGCAACA GAAATCTATC
1261 TCACAGCTAC AGACCTCAAA AGGCTGATCA GCAAAGCACT AGAGGAAGAA CAATCTTTGG
1321 ATGTGGGGGA AATTCAGTTC ACTGATGAAA TTGCTGGATC ACTGCCAGCC TTGGCTCCTG
1381 AACCCCAACT AGAGCTGCCC ACATCTTTTG CTGTTATAAC AGAGGATGCT ACTTTGAGTC
1441 CAGAACTTCC TCCTGTTGAA CCCAGCTTG AGACAGTGGG CCGAGCAGAG CATGGCTAC
1501 CTGACCTTCT TTGGTCTCCA CCTGCTATGG CCTACCTTCC CTGTCAGAAG CTCACCTTT
1561 CTTTATGGCA TCAACATCT TCTCTCTGAC TGATCAAGGC GATGACGATA CAATGGCCAC
1621 TGACCAGACA ATGCTAGTAC CAGGGCTCAC CATCCCCACC AGTGATTATT CTGCAATCAG
1681 CCAACTGGCT CTGGGAATTT CACATCCACC TGCATCTTCA GATGACAGGC GATCAAGTGC
1741 AGGTGGCGAA GGTATGGACA GAGACCTAGA TGAATGGAT CTGCTGACA CTCCTGCCCC
1801 ATCTGAGGTA CCAGAGCTCA CGGAATATGT TTCTGTCCCA GATCACTTTCT TGGAGGATAC
1861 CACTCTGGTC TCAGCTTTAC AGTATATCAC CACTAGTTCT ACTGATTCTT CCCCCAAGG
1921 CCGAGAGCTG GTAGTGTTCT TCAGTCTGCG TGTGCTAAC ATGGCCCTTCT CCAACGACCT
1981 GTTCCAACAG AGCTATTGAG AGTACCGAGC TCTGGAGCAA CAATTGCTGGT CCACTGCTGT
2041 TCCATATCTA CGATCCAATC TTACAGGATT TAAGCAACTT GAAATACTTA ACTTCAGAAA
2101 CGGGAGTGTG ATGTGGAATA GCAAAATGAA GTTTGCTAAG CATGCGCGT ATAACCTCAC
2161 CAAGGCTGTG CACGGGGTCT TGGAGGATT TCGTTCTGCT GCAGCCCAAC AACTCCATCT
2221 GGAAATAGAC AGCTACTCTC TCCC
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SEQ ID NO: 6 Human IPM 150 amino acid sequence, isoform C

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1 MYLETRRAIF VWFIFLQVQG TKDISINIH SETKDIDNPP RNETTESTEK MYKMSTMRI
61 FDLAKHRTKR SAFFPTGVKV CPQESMKQIL DSLQAYYRLR VQEAWEAY RIFLDRIPTD
121 GEYQDWSVIC QQETFLCFDI GKNFSNSQEH LDLQRIKQ RSFPDRKDEI SAEKTLGEPG
181 ETIVISTAIY ISKTWAVF
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SEQ ID NO: 7 Human IMPG1 gene, regulatory region

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1 AGGGTGTAGG CTTTGAACC AGGACTCTTT AGGTTTAAAT CCTAGCTCTG CCACATATAC
61 TTTATCTCCC TCAAAATTTAA AAGAGATAGT ATTAACAGTG TTTATATTGT CATATTGAGG
121 ATCATATGGA TAATCTATGG ACATCTCTAA GAACAATGTC TATCCACAAC ACAAGGCTC
181 AATATACAGT AGTAGTTGCA GTGTGTTTCA TGACTCAGCA ATATGTAGCA TGTATAGTCA
241 AAATATATA AAATCAAATA TTCAAAAACT GAAATTACAA TAATCTGAT GAAGAAAGAT
301 GGAAAGATGT TTACAATGAG TAGAAAGGGT ATGTGTGGAA GTGAAGTTAT TCTCAATATC
361 TATTATTGTA TAATACCTAA AAGTGAAAC CTCCAAAATA CTAATAGAGG CATGTTATTT
421 AGAAGTGCAA ATGAGACTAC TAGAAGAAAT AGGTTGATGA AGTAAAAATG GCTCCCCCTT
481 GAAAGAAGCA ATGGGTAGAA GAAAGGCACA ATTTTCTCTG ACAAACTTTG TAGAAAAAAA
541 GTATTTGACC CCTTAACAC AGTGATACA GATTTTAAAC ATTTAAACCA GACTTAAATC
601 AAAAAAGCCA CCGTATGTA ATTCAAAATC AAAAGCAATT TATAAGCAG AACATAAGG
661 AGAATGGAGA CAGTTTCGCT ATCTGTGGAG ACTAATACAT ATTGGATAAC CATATACTTT
721 CAGGCAGACA AATTAAGCTC TTTTAATGGA TGTTTCTGTG ACATGCTGAT TTAGAAAAAC
781 CTGACCCCTA ATGGTCAGCC TTATCTCTG TTTGGCAGAA CTTCCTGCTG CTCTCTGTGT
841 CACTGTAAAC GGTGAATAAC TAAGAAAAAA CTGTGCTGTG AGACACTTGT TTATAATGGC
901 ATTCAGGGTC CTGGAGCTAG GCTGACAGAT GCTCCTCCAG AAGGTTAATG AGATAAAGGT
961 TCCTCAGCTG GGCCCTTAAG CAGAGATTAC ACCTGAGGGA AAGACAAGCA GATTATTCCA
1021 GAAACAGACA GCTCTACATG TTCTTCATAA ATTAACACCC CATATAAGGT AAACCAAGAA
1081 GGTATCTCTC AATCACTCGG TATCAATATA TAATTATTTT CACATTTTCT GTTACTTTTT
1141 AATGAGATTG GAGGTGTTTC TGTGATTGTT ATCAGAATTA CCAATGCGAA AAAGCCAGAA
1201 TGTATTTGGA AACTAGAAGA GCTATTTTTG TTTTGTGGAT TTTTCTCCAA GTTCAAGGAA
1261 CCAAGGTAA GTTACTTAAA TGTTTACTTT TAAATTGCTT ATCTATAAAA TCTACCATA

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1321 GAAGTGAATA TTTAGAACCA ACAAGGCTAC CAATTTATCT CACGGGCTAG TATATAGTAG
1381 GCCTTGAATA AATATTGCTT GATTGATTGA ATAATTAACAT ATCAGAAATG ATTTTCACTT
1441 GATTTAATAT TTACTACATG GTCTTAAGTG CAGTGAAGAT TAACAAAATA GGAGAGATGA
1501 ATGATCTCTTA TTTGCTGTTC TAAACATTTC ATTGAAAATT CTTATTATTA AATGTAAATA
1561 NTATTAGTAG ATCTGGTGAA AACTAAACTC CATTTATCCA CCCCAAAATC AACCAATAAA
1621 AACCTAAAGG ATCAAAGTAA TGTTTTAAGT CATTTATGGT CAGACAAAAA AAAGTAAGTA
1681 TTTCTTACCT TCTCACAATG AAATCATGAG TTGCTTTCCC TTAGAAAATA CCAACATTCT
1741 TTCATCTTCA GGGTTCATGA TGACAACAC TTCAAAATTT GGTGTGTTTT GAAAGTTGTA
1801 CGCATAAAG AACTAGGCAA TGTATGTTCT TATGGCAAT CTGCATCTGA ATATGAAA
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SEQ ID NO: 8 Mouse IPM 150 cDNA sequence, isoform A

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1 ACAAGATTAT TCCAGGAAC TACCTGCTTC CGGATCTCTG AGAATTAGCA CCTTCATAGG
61 GTAAACCAGG GAGGTCGTCT GTACTCAGCC GGCACCTGGA TTTGATTATT TTTTCATATT
121 CAGTCACCTT ATCTCTTTAA GTGTGACTTG GTATTGTTCT GTGATTTTTC AGAATTACCA
181 GTATACAGAA CAGAATGAA TTTTCAAATT AAACATGCTA TCTTTGTTTT TGGGATTTTT
241 CTCCAAGTTC AAGGAATCAA AGATACCTCT ATTTAAATAT TCAGTTCTGA AATTA AAAAC
201 ATAGACAAAA CCCCAGAAT CAAAAACAAT GAAAGTACTT CAACAGTGCA CAAAGTGTC
361 ACCATGAACG GAATATTGCA TTTGCCAAAG CTTCGAACCA AAAGATCAGC ACTTTTCCCA
421 GCTGCTAAAC TCTGTCCACA GGAATCCTTG AGACAGATTT TAGCAAGTCT TCAAGAATAT
481 TATAGACTGA GAGTATGTCA AGAAGTCGTG TGGGAAGCAT ATCTGATCTT TCTGGACCGA
541 ATTCCTGACA CAGAGGAATA TCAAGACTGG GTCAGCTCTC GCCAGAAAGA AACCTTCTGC
601 CTCCTTGACA TTGGGAAAAA CTTCAGCAAC TCCAGGAGGC ACCTAGATCT TCTTCAGCAG
661 AGAATAAAAC AGAGAAGCTT CCTGGGAGG AAAGATGAGA CAGCTCCATC GGAGCACTG
721 GAAGCACCTA CTGAAGCCCC TGTGGTACCC ACAGATGTTT CCAGGATGTC CCTGGGCCCC
781 TTCCCACTTC CTCTCGATGA CACAGACCTC AAGGAGATTC CACTGTGTCAC CCTCAGGAG
841 ATTTCAAAGC CCACAACAGA AAGTAAACCA GAACCTATTC ACGTGTCTGA ATTCTCATCA
901 GAGGAGAAGG TCGGAATTCAG CATCTCTCTG CCAAACACCA GGTTCAGGCG AGAGCTCACC
961 AACTCTGGGT CACCATACTA CCAGGAACGT GTGGGACAGT CCAAATCTGA GTTGCAAAAG
1021 ATATTTAAGA AACTTCCAGG ATTCGGAGAA ATCCGTGTAT TAGGATTTAG ACCAAAGAAA
1081 GAAGAAGATG GTTCAAGCTC CACAGAAATA CAGCTTATGG CCATCTTTAA GAGGGACCAT
1141 GCAGAAGCAA AAAGCCCTGA TAGTCATCTA CTGCTCTCTG ATTTCCAACAA AATTGAAAGT
1201 GAAAGAATCC ATCATGGAGT CATAGAAGAC AAACAACACG AAACCTACCT CAGGCTACAA
1261 GACCTCAAAA AACTCATCAT ACAACTACTA GATGGAGACC TGTCCTTGGT AGAAGGGAAA
1321 ATTCCTATCG GTGATGAAGT TACTGGGACA CTCTTCAGAC CTGTCACTGA ACAGATCTG
1381 CCCAAGCCCC TTGCTGATGT CACAGAGGAT GCCACTTTGA GTCCAGAACT TCTTTTCGT
1441 GAGCCTAGGCG TTGAGGCAGT GGACAGAGAA GGATCTGAGC TGCCTGGAAT GTCTCCAAA
1501 GACAGTCTTT GGTCTCCACC TGTATCAGCC TCAATTTCCC ATCAGTGAATA TCACTCTCG
1561 TTTACACCTA GCATCTTCTC TCTAGATGCT CAAAGCCCCC TCCCTTGTAT GACCACTGGC
1621 CCAACAGCAC TCATCCCCAA GCCCACTCTC CCACATATCG ATTTATCTAC TACTCCGCAA
1681 TTGCCTCTGG AATCGTCACA TTGGCCTGCA TCCTCCAGTG ACAGAGAGCT GATCACAAGC
1741 AGCCATGACA CAATCCGAGA CCTAGATGGC ATGGATGTGT GTGCACGCC ATGCTTTGTA
1801 GAAATATCAG AACTGAGTGG ATACGATTCT GCCTCGGGTC AGTTCTTTGA GATGACCACA
1861 CCAATCCCCA CAGTACGGTT CATCACACC AGCTCCGAGA CATTGGCCAC GAGGGCCAG
1921 GAGCTAGTGG TATTTCTCAG CCTGCGTGT GTAAACATGC CGTTCTCCTA TGACCTGTTT
1981 AACAGAAGTT CTCTGGAGTA TCAAGCCCTG GAACAACGAT TCTCAGACTC CTGGTTTCCC
2041 TATCTACGAT CGAATCTTAC GGGATTTAAG CAACTGGAAG TACTCAGCTT CAGAAACGGA
2101 AGTGTGATGC TGAACAGCAA AGTGGCGGTT GCAAAGGCGG TACCTACAAA CCTCACCCAG
2161 GCGGTGCGCG GGGTCTTGGA GGATCTTCGG TCCACCCGAG TCCAGGAGCT CAATCTGGAA
2221 ATCGAAAGAT ACTCCCTCGA CATTGAACCA GCTGATCAGG CGGATCCCTG CAAACTCTTA
2281 GACTGTGGCA AATTTGCCCA GTGTGTAAGG AATGAGTGGA CAGAGGAAGC AAGAGTGTCC
2341 TCGAGACAGG GAGCATGAGG CCACGGGACC CTGGAATACC AGACCCCTGA CCTCTGCCC
2401 CTTGGAAAAA CTTGTGTGGC CGGCCGAGAA CCAAGCACTC ATGCAGGCC AACAGATCAC
2461 TCTACAAACC AAGCTCAGGA ACCTGGTGT AAAAAGTATC GTACAGAAAA TAAGGTAGTC
2521 AAGAAGAAAG AATTTAAACT ATCAGCTATA GGATTTGAAG AATTTGAAAG CACGAGCTGG
2581 GAGGGAAATT AAAAGCTGGA ATCATATGCA TTATGTTGCA AACTCTGTTG AAAGGAAACT

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2641 TTATTTCTTA AAGAAAGGTG TATCTGTTCT GTTAACCTTC GAAAAACAGA GGGAGAGATT
2701 CACTGGTCAT TGGAAATACG GCATGTAATC AACTTTGAGA CTCAGCATGG TTGAACAAGA
2761 GCACAGGCGT GTATTTTGATG ACAGTTAAGC CTGGTGGGGG CGGGGGGCGC ATATTTTGTAG
2821 TCAAAACTCA AAGCAATCAT TGGAAACACAT TTGACTATTT TTGGACAGAT CTCGAAGTAGC
2881 AAGAGATAAGG TTAGCTTTTT TCTTCTTTTA AATTATTACA TAAARCTTAT TCAAAATAAA
2941 TACAACTTGT TTAGTGGGTT GTACAAATATT GAGGATCTGA TTCTTTTATA TGTGTAGAAAT
3001 TACAGTTAAA AGATTATCAT TTGGGCCAGA GAGATAGCTA AGTGGTTAAG AGTATATACT
3061 GCTCTTCCAG AAGCCCTGGG TTTACCGTCC CAACAGCCAC ATTGACTGGC TCACACACAC
3121 CTGTAAGTCA GGCCTCCAGAG AACAAACACC CTCCTCTGGC CTTTGTACCC ACGTGCACAT
3181 AACCGCAAC AGACACACCC ACGCTATTTT TTTAGAAGTC ATTTGATTTT TTAATTAGGG
3241 GTGGAAGAAC AGGCTGGAGA GATGACTCCG TGGTTAAGAA CAGTGTGTTG TCTTCCAGAG
3301 GACCCAGGTT CAGTTCACAG AACCCACAAG GCNAGTCTCC CAACTATTCA TAATTCTAGT
3361 TCAAGTGGAT CCAGCACCCCT CTCTAACTG ATACTGCCAG TACCAGGCAG CCATGTGGTG
3421 CATATGCATT TGGGCAGGTA AAACACTCAG ACACGCAAAA AATTTTAAAT CTAATATTTTG
3481 AAAATATTTT AGTTTTAAGG ATGATCACTG TGTGAGGGTC AGGTCTCTTA TGTATGAATT
3541 TAGTACCAAG AACTGTGATG AGTATATGTA TGCTCCATTC TATAGTCTCT TCTCTCTCTC
3601 TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTGGAAT TCCGGAATTC CGGAATTCGC
3661 GAATTCGG
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SEQ ID NO: 9 Mouse IPM 150 amino acid sequence, isoform A

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1 MNFIQKHAIF VVFIQLVQVG IKDTSIKIFS SEIKNIDKTP RIETIESTST VHKVSTMKRI
61 FDLPKLRTKR SALFPAANIC PQESLRQILA SLQEYRRLRV CQEVVWEAYR IFLDRIPDTE
121 EYQDWVSLCQ KETFCLFDIG KNFSNSQEHL DLLQRIKQKR SFPGRKDETA SMETLEAPTE
181 APVVPTDVSR MSLGPPFLPS DDTDLKEIHL VTLKDQIKPT TESKTEPIHV SEFSSEKVE
241 FSIISLPHNR KAELTNSGSP YYQELVGSQJ LQLQKIFKFL PGFGEIRVLG FRPKKEEDGS
301 SSTIEQLMAI FKRIEHAEXS PDSHLLSLDS NKIESERIHH VGEDKQKET YLTATDLKKL
361 IILQLDGLDS LVEGKIPFGD EVTGLTFRPV TEPDLPRPLA DVTEDATLSP ELFPVPEPRLE
421 AVDREGSELP GMSKSDSWWS PPVSASISRS ENLPSFTPSI FSLDAQSPPP LMTTGPTALI
481 PKPTLPTIDY STIRQLPLES SHWPASSSDR ELITSSHDTI RDLGDMVDSD TPALSEISEL
541 SGYDSASGQF LEMTTPIPTV RFITTSSETI ATKQGLVWF FSLRVANMPF SYDLFNKSSL
601 EYQALEQRFT DLLVPLYLRSN LTGFKQLEIL SFRNGSVIVN SKVRFAKAVP YNLQAVRGV
661 LEDLRSTAAQ LDCLEIESYS LDIEPADQAD PCKLLDGCXF AQCWNKEWT EAECCRCRQH
721 ESHGTLDYQT LNLCPGKTC VAGREQATPC RPPDHSTNQA QEPGVKKLRQ QNKVVKKRNS
781 KLSAIGFEFF EDQDWEGN
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SEQ ID NO:10 Mouse IPM 150 cDNA sequence, isoform D

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1 GGCTTTAAAC CAGGAGGGTC GTCTGTACTC AGCGGGCACC TGGATTGTAT TATTTTTCAT
61 ATTTTCAGTCA CCTTATTCTT TTAAGTGTGA CTGGTATTG TTCTGTGATT TTTCAAGAAAT
121 ACCAGATATAC AGAACACAGAA TGAATTTTCA AATTAACATG GCTATCTTTG TTTTGGGAT
181 TTTTCTCCAA GTCACAGGAA TCAAGATATG TCAAGAAATC GTGTGGGAAG CATATCGTAT
241 CTTTCTGGAC CGAATTCTCG ACACAGAGGA ATATCAAGAC TGGGTGACCC TCTGCCAGAA
301 AGAAACCTTC TGCTCTTTTG ACATTGGGAA AAACCTCAGC AACTCCGAGG AGCATCTAGA
361 TCTTCTTACG CAGAGAAATA ACACAGAGAAG CTTCCTGGG AGGAAAGATG AGACACGCTC
421 CATGGAGACA CTGGAAGCAC CTACTGAAGC CTTCTGTGTA CCCACAGATG TTTCCAGGAT
481 GTCCTCTGGG CCATTCCAC TTTCTTCTGA TGACACAGAC CTCAGAGAGA TTCTCAGTGT
541 CACCTCTAAG GACATTCAAA AGCCCAACAC ACAGAACCTA ACAGACCTTA TTCAAGTGTG
601 TGAATTCTCA TCAGAGGAGA AGGTGGAGTT CAGCATCTCT CTGCGAAACC ACAGGTTCAA
661 GCGAGAGCTC ACCAACTCTG GGTCAACATA CTACACAGAA CTGGTGGGAG AGTCCCACT
721 GCAGTTGCAA AAGATATTTA AGAAACTTCC AGGATTGCGA GAAATCCGCT TATTAGGATT
781 TAGACCAAGG AAAGAAGAAG ATGGTTCAAG CTCACAGAAA ATACAGCTTA TGGCATCTT
841 TAAGAGGGAC CATGCAGAGG CAAAAGGCCG TGATAGTCAT CTACTGTCTC TTGATTCCAA
901 CAAAATTGAA AGTGAAGAAA TCCATCATGG AGTCATAGAA GACAAACAC CAGAAACCTA

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961 CCTCACAGCT ACAGACCTCA AAAAAGCTCAT CATAACAATA CTAGATGGAG ACCTGTCTCT
 1021 GGTAGAAGGG AAAATTCAT TCGGTGATGA AGTTACTGGG ACACCTCTCA GACCTGTCCAC
 1081 TGAACACAGT TCGCCCAAGC CCCTTGCTGA TGTACACAGAG GATGCCACTT TGAGTCCAGA
 1141 ACTTCTCTTTT GTTGAGCCTA GGTGTGAGGC AGTGACACAGA GAAGGATCTG AGCTGCCTGC
 1201 TGATCAGGCG GATCCCTGCA AACTTCTAGA CTGTGGCAAA TTTGCCAGCT GTGTAAAGAA
 1261 TGAGTGGACA GAGGAAGCAG AGTGTCCGTG CAGACAGGGA CATGAGAGCC ACCGGGACCTC
 1321 GGACTACACG ACCTCGAAC CTTGTCCCCC TGGAAAGACT TGTGTGGCCG GCCGAGAACA
 1381 AGCAACTCCA TCGAGGCCAA CAGATCACTC TACAAACCAA GCTCAGGAAC CTGGTGTATA
 1441 AAAGCTACGT GAGCAAAATA AGGTAGTCAA GAAAAGAAAT TCTAAACTAT CAGCTATAGG
 1501 ATTTGAAGAA TTCTGAAGACC AGGACTGGGA GGGAAATTA AAGCTGGAAT CATATGCAAT
 1561 ATGTTGCAAA CTCTGTTGAA AGGAAACTTT ATTCTTAAA AAAGGTGTA TCTGTTCTGT
 1621 TAACCTCTGA AAAACAGAGG GAGAGATTCA GTGGTCATTG GAATACAGGC ATGTAATCAA
 1681 CTTTGAGACT CAGCATGCTT GAACAAGAGC ACAGGCGTGT ATTTGA

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SEQ ID NO:11 Mouse IPM 150 amino acid sequence, isoform D

1 MNFQIKHAIF VFGIFLQVQG IKVCQEVVWE AYRIFLD RIP DTEEYQDWVS LQKETFCFLF
 61 DIGKNFSNSQ EHLDLLQQR I KQSFPGPKRD ETASMETLEA PTEAPVLPD VSRMSLGPFP
 121 LPSDDTDLKE ILSVTLKDIQ KPTTESITEP IHVSEFSSEE KVEFISLPLN HRFKAELTNS
 181 GSPYYQELVG QSLQLQKIF KKLPGFGEIR VLGRFPKKEE DSSSTIEQL MAIFKRDAE
 241 AKSPDSHLLS LDSNKIESER IHHGVIEDKQ PETYLATD LKKLIQLLDG DLSLVEGKITP
 301 FGDEVGTGLF RPVTPEPLPK PLADVTEDAT LSPELPFVEP RLEAVDREGS ELPADQADPC
 361 KLLDCGKFAK CKNEWTEEA ECRCRQHEH HGTLDYQLN LCPGPKTCVA GREQATPCRP
 TDHSTNQAQE PGVKLRQQN KVVKKRNSKL SAIGFEEDF QDWEFN

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SEQ ID NO:12 Mouse IPM 150 cDNA sequence, isoform E

1 TCTGCAGAAT TCGGCTTAAC CAGGGAGGTC GTCTGTAATC AGCCGGCACC TGGATTGTAT
 61 TATTTTTTCAT ATTTCACTCA CTTATTTCT TTAAGTGTGA CTTGGTATTG TTCTGTGATT
 121 TTTTCAGAAT ACCAGTATAC AGAACCAGAA TGAATTTTCA AATTAACACT GCTATCTTTG
 181 TTTTGGGAT TTTTCTCCAA GTTCAAGGAA TCAAAAGTAT CTTCTATTAA ATATTCACTG
 241 CTGAATTTAA AATCATAGAC AAAACCCCAA GAATCGAAAC AATTGAAAGT ACTTCAACAG
 301 TGCAACAAAT GTCAACCATG AAACGCCAGC CTTGTAGAAA ATATCGAACG TTAGTGGATA
 361 CGATTCTGCC TCGGGTCAGT TCTTGAGAT GACCACACCC ATCCCAACAG TACGGTTCAT
 421 CACCACAGC TCCGAGACCA TTGCCACCAA GGGCCAGGAG CTAGTGGTAT TTTTCAGCCT
 481 GCGTGTGTGT AAGTCGCGT TCTCTATGA CCTGTTCAAC CAGAGTTCTC TGAAGTATCA
 541 AGCCCTGGAA CAACGATTCA CAGACCTGCT GGTTCCTCAT CWACGATCGA ATCTTACGGG
 601 ATTTAAGCAA CTGGAATATC TCAGCTTCAG AAACGGAAAT GTGATCGTGA ACAGCAAAGT
 661 CGGGTTTGCA AAGGCGGTAC CCTACAACCT CACCACAGGC GTGCGCGGGT TCTTGGAGGA
 721 TCTTCGGTCC ACCGCACTC AAGGGCTCAA TCTGGAATC GAAAGCTACT CCTCCGACAT
 781 TGAACAGCTG GATCAGGCGG ATCCCTGCAA ACTTCTAGAC TGTGGCAAA TTTGCCAGTG
 841 TGTAAGAAT GAGTGGACAG AGGAAGCAGA GTGTCTGTC AGACAGGAC ATGAGAGCCA
 901 CGGGACCTTG GACTACCAGA CCTGAACCT CTGTCCCCCT GGAAAGACTT GTGTGGCCGG
 961 CCGAGAACAA CCACTCCAT CGAGGCCACC AGCACTCTCT ACAAACCAAG CTCAGGAACC
 1021 TGTGTGTTAA AGCTACGTC AGCAAAATAA GGTAAGTCAAG AAACGAAAT CTAACATATC
 1081 AGCTATAGTA TTTGAAAAAT TTGAAGACCA GGACTGGGAG GGAAATTTAA AGCTGGAATC
 1141 ATATGATGTA TGTGTCAAC TCTGTTGAAA GGAAACTTTA AAAGGTGTAT
 1201 CTGTCTCTGT AACTTCTGAA AAACAGAGGG AGAGATTACG TGGTCAATGG AATACAGGCA
 1261 TGTAAATCAK TTTGAGACTC AGCATGCTTG AACAGAGACA CAGGCGTGTA TTTGATAAGC
 1321 C

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SEQ ID NO:13 Mouse IPM 150 amino acid sequence, isoform E

1 MNFQIKHAIF VGFIFLQVQG IKDTSIKIFS SEIKNIDKTP RIETIESTST VHKVSTMKRQ
61 PCQKYQN
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SEQ ID NO:14 Monkey IPM 150 cDNA (partial)

1 ATTTTCTTTC CGAAGCGGGT TAAAGTCTGT CCACAGGAAT CCATGAAACA GATTTTAGCC
61 AGTCTTCAAG CTTATTATAG ATTGAGAGTG TGTCAGGAAG CAGTATGGGA AGCATATCGG
121 ATCTTTCTGG ATCGCATCCC TGACACAGGG GAATATCAGG ACTGGGTGAG CTTCTGCCAG
181 CAGGAGACCT TCTGCCTCTT TGACATCGGA CAAAACCTCA GCAATTCCTA GGAGCACCCT
241 GATCTTCTCC AGCAGAGAAT AAAACAGAGA AGTTTCCCTG AGAGAAAAGA TGAAGTATCT
301 ACAGAGAAGA CATTGGGAGA GCCTAGTGAA ACCATTGTGG TTTCAACAGA TGTGGCCAGC
361 GTCTCACTTG GGGCTTTCCC TGTCACCTCT GATGACACCC TCCTCAATGA AATTCTCGAT
421 AATGCACTCA ACGACACCAA GATGCCTACA ACAGAAAAGG AAACAGAACT CGCTGTGTCT
481 GAGGAGCAGA GGGTGGAGCT CAGCATCTCT CTGATAAACC AGAGGTTCAA GGCAGAGCTC
541 GCTGACTCTC AGTCA
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SEQ ID NO:15 Monkey IPM 150 amino acid sequence (partial)

1 IFFPNGVKVC PQESMKQILA SLQAYYRLRV CQEAWEAYR IFLDRIPDTG EYQDWSVFCQ
61 QETFCFLDIG QNFSNSQEHL DLLQRIKQR SFPERKDEVS TEKTLGEPSE TIVVSTDVAS
121 VSLGPPFPVP DDTLLNEILD NALNDTKMPT TERETELAVS EEQRVELSIS LINQRFKAEI
181 ADSQS
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SEQ ID NO:16 Human IPM 200 (isoform A) cDNA

1 CGGGCTACTT TGAAGGACA ACCATTTTTC TTTCCTGCTAA TTTATAATGG TTTTGAAGTG
61 GTTGTTTCATT CTCAAACATA GACCTTTTAA TGTAGGTGCT TTCTCTATAAC TCCTTTGTTAT
121 TGGAAAGTTTC AAGGATTTGG AACTCAATT AAGGATCTCT TCCTCTCCTC ATTCTTTTGG
181 TTTTGGCCCA AATGATTATG TTTCTCTCTT TTGGGAAGAT TTCTCTGGGT ATTTTGATAT
241 TTGTCTGAT AGAAGGAGAC TTTCCATCAT TAACAGCACA AACCTACTTA TCTATAGAGG
301 AGATCCAAGA ACCCAAGAGT GCAGTTTCTT TTCTCTGCTC TGAAGAATCA ACAGACCTTT
361 CTCTAGCTAC CAAAAGAAA CAGCCTCTGG ACCGCAGAGA AACTGAAAGA CAGTGGTTAA
421 TCAGAAGGCG GAGATCTATT CTGTTTCCCTA ATGGAGTGAA AATCTGCCA GATGAAAGTG
481 TTGCAGAGCG TTGCGCAAT CATGTGAAGT ATTTTAAAGT CCGAGTGTGT CAGGAAGCTG
541 TCTGGGAAGC CTTCAGGACT TTTTGGGATC GACTTCTCTGG GCGTGAGGAA TATCATTA
601 GGATGAATTT GTGTGAGGAT GGAGTCACAA GTATATTGTA AATGGGCACA AATTTTAGTG
661 AATCTGTGGG ACATAGAAGC TTAATCATGA AGAAACTGAC TTATGCAAGG GAAACTGTAA
721 GCAGCTCTGA ACTGCTCTCT CCAGTTCCTG TTGGTGATAC TTCAACATTG GGAGACACTA
781 CTCTCAGTGT TCCACATCCA GAGGTGGACG CCTATGAAGG TGCCCTCAGG AGGAGCTTGG
841 AAAGGCCAGA GGAGAGTATT AGCAATGAAA TTGAGAATGT GATAGAAGAA GCCACAAAAC
901 CAGCAGGTGA ACAGATTGCA GAATTCAGTA TCCACCTTTT GGGGAAGCAG TACAGGGAAG
961 AACTCAGAGA TTTCTCCAGC TTTACCACC AGCACCTTGA AGAAGATTTT ATTTTCAAGG
1021 TTGAAATGCG ATTTACTGGG TTACCAGGCT TCGTGTACTT GAATTTAGGT
1081 CCCCCAAGGA AATACAGAGT GGCCTAGATG TTTACTATGC AGTTACCTTC AATGGTGAGG
1141 CCATCAGCAA TAACCTCTGG GACCTCATTA CAACAAGGTG GAAACCATGT
1201 GCCTTGTGGA ACTGGATGAT AAACCCACTG TTGTTTATAC AATCAGTAAC TCCAGATATT
1261 ATATTGCTGA GCATTGTCAG CAGAATTTTT TGCTGGGGAA CTCTTCTCTG AATCCAGATC
1321 CTAGTTTCTC CGAGCTTATC AATGTGAGAG GAGTTTGTGC TCACCAAACT GAAGACTCTAG
1381 TTTGGAACAC CCAAGGTTCA AGTCTTCAGG CAACGCCGCT ATCTATTCTG GATAATACCT
1441 TTTCAAGCTGC ATGGCCCTCA GCAGATGAAT CAGTATTCCA CCACTTGATT
1501 TCAGCTCTGG TCCTCCTCTA GCCACTGGCA GGGAACTCTG GTCAGAAAGT CCTTTGGGTG


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1561 ATTTAGTGTG TACACACAAA TTAGCCTTTC CCTCGAAGAT GGGCCTCAGC TCTTCCCCAG
1621 AGGTTTTAGA GGTTAGCAGC TTGACTCTTC ATTCTGTAC CCCTGAGCTG CTTCAGACTG
1681 GCTTGCCCTGT GGCTTCTGAG GAAAGGACTT CTGGATCTCA CTGTGGTAGA GATGGATTAG
1741 CCAATGTTGA AGAGTCAGAA GATTTTCTTT CTATTGATTC ATTCGCTTCA AGTTTCATTCA
1801 CTCAACCTGT GCCAAAAGAA ACAATACCAT CCATGGAAGA CTCTGATGTG TCCTTAACAT
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1921 AAGACCAATT AAAAGTAGGC CTTTCTCTGC CAGATGCATC CATGGAAAAA GAGTTAATAT
1981 TTGACGGTGG TTTAGGTTCA GGGTCTGGGC AAAAGGTAGA TCTGATTACT TGGCCATGGA
2041 GTGAGCTTTC ATCAGAGAAG AGCGCCGAAC CACTGTCCAA GCCTGGCTTG GAAGTGAATG
2101 ATTCACTTTT GCCAGCTGAG ATTTAAGACA AGAACTAGT TTAGTGTGAC AAAATGGATT
2161 CCACAGACAA ACTTAGTAAG CACTCAAAAT ATGAACATGA TCAGAGTCC ACACACTTTC
2221 CAGAGGAAGA GCCTCTTAGT GGGCTCTGCT TCCCCATCTT CGCAGATACT GCAGCTGAAT
2281 CTGCGTCTCT AACCCCTCCC AAGCACATAT CAGAAGTACC TGGTGTGTAT GATTGCTCAG
2341 TTACCAAAAG ACCTCTTATA CTGACATCTG TAGCAATCTC TGCCCTCACT GATAAATCAG
2401 ATCAGGCAGA TCCCATCTTA AGGGAGGATA TGGAACAAA TACTGAGTCA TCCAACATAT
2461 AATGGTTTGA CGTGAGGTT TCAATGGTAA AGCCAGATAT GCAAACTTTG TGGCACTATG
2521 TGCCAGAACT AGAGAGAGTT TGGACAAGAA CTCTCTCCCT AGAGAAATGT TCCAGAGACA
2581 ATTTGGCAAG TACACACAG AGTGTCTGACA GGCTCTGGTT ATCTGTGACA CAGTCTACCA
2641 AATTGGCTCC AACCACAATC TCCACCCTGC TAGAGGATGA AGTAATTATG GGTGTACAGG
2701 ATATTTCGTT ACCACTGGAC CGGATAGGCA CAGATTACTA CCAGCTTGAG GAAGTCCAA
2761 AGCAAAATGC CAAGGTGGGT AGTTATGTGG AAATGTCAAC AAGTGTTCAC TCCACAGAGA
2821 TGGTTAGTGT GGCTTGGCCT ACAGAAGGAG GAGATGACTT GAGTTATACC CAGACTCTAG
2881 GAGCTTTGGT GGTTTTCTTC AGCCTCCGAG TGAATAACAT GATGTTTTC GAAGATCTGT
2941 TTAATAAAAA CTCTCTGGAG TATAAGCCC TGGAGCAAAG ATTCTTAGAA TTGCTGGTGT
3001 CCTATCTCCA GCAAAATCTC ACGGGGTTC AGAACTTAGA AATCCTCAAC TCCAGAAATG
3061 GCAGCATTTG GGTGAACAGT CGAATGAAGT TTGCCAATTC TGTCCTCTCT AACGTCAACA
3121 ATCCGGTGTA CTGATTCTG GAAGACTTTT GTACCAATTC TACAATATCC ATGAACATGG
3181 CTATTGATAA ATACTCTCTT GATGTGGAAT CAGGTGATGA AGCCCAACCT TGCAAGTTTC
3241 AGGCGTGTA TGAATTTTCA GAGTGTCTGG TCAACCCCTG TCACAGTGAA GCAAGGTGCA
3301 GATGCTTCCC TGATACCCTG AGTGTGGAAG AACGGCCCTG TCAGAGTCTC TGTGACCTAC
3361 AGCCTGACTT CTGCTTGAAT GATGGAAAGT GTGACATTAT GCCTGGGCAC GGGGCCATTT
3421 GTAGGTGCCG GGTGGGTGAG AACTGGTGGT ACCGAGGCAA GCACCTGTGAG GAATTTGTGT
3481 CTGAGCCCGT GATCATAGGC ATCACTATTG CCTCCGTGGT TGACTTCTT GTCATCTTTT
3541 CTGCTATCAT CTACTCTTC ATCAGGACTC TTCAAGCACA CCATGACAGG AGTGAAGAG
3601 AGAGTCCCTT CAGTGCGCTC AGCAGGCAGC CTGACAGCCT CTGATCTATT GAGAAATGCT
3661 TGAAGTACAA CCCCGTGTAT GAAAGTCACA GGGCTGGATG TCGAAGATAT GAGGGACCTT
3721 ATCTCAGACA TCCCTCTTAC AGCTCTGCTA GCGGAGACGT GATTGGTGGG CTGAGCAGAG
3781 AAGAAATACG ACAGATGTAT GAGAGCAGTG AGCTTTCCAG AGCTGAAATT CAAGAGAGAA
3841 TGAGAGTTTG GGAACGTGAT GCCAATGATC CTGAGTTTGC AGCTTTTGTG AGAGAGCAAC
3901 AAGTGGGAAG GTTTLTAACA AAACCTCTGT TCTGAACTG ATTAGAAGCC TGGAGAAGAT
3961 GGAGATTACT TGTTACTTAT GTCATATAAT TAACCTGGAT TTTAACTACT GTTGGGAAGA
4021 WPGATTTTCTA TGAAAAAAAT AAATATAGGG CACACTGTMT TTTTTCAGC TTAAGTTTTC
4081 AGAATGTAGT AAGAGATGTT ACCATTTTTA TTTCTATAAA GACTGAATGC TGTGTTTAAA
4141 TAAATTGAAA ACTACGTAAA AAAAAA
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SEQ ID NO:17

Human IPM 200 amino acid sequence, isoform A

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1 MIMFPLFGKI SLGILIFVLI EGDFPSLTAQ TYLSIEIQE PKSASVSLFP EESTDLSLAT
61 KKKQPLDRRE TERQWLIRRR RSILFPNGVK ICPDESVAEA VANHVYKFKV RVQOEAVWEA
121 FRTFWDRPLP REEYHYWMNL CEDGVTSIFE MGTNFSSEVE HRSILIMKLT YKATVSSE
181 LSSVPVPGDT STLGDTTLSV PHPEVDAYEG ASESSLERPE ESISSELEHN YEATKPAGE
241 QIAEFSIHLH GKQYREELQD SSSFHHQLES EEFISEVENA FTGLPGYKEI RVLEFRSPKE
301 NDSGVDDVYYA VTYGFEAISN TTWDLISLHS NKVENHGLVE LDDKPTVVYT ISNFRDYIAE
361 TLQQNFFLLG SSNLNPPDPSL QLINVRGVL R HQTEDLVWNT QSSSLQATPS SILDNFTFQA
421 WPSADESITS SIPPDLDFSSG PPSATGRELW SESPLGDVLS THKLAFPSKM GLSSSPVELE
481 VSSLTHSVT PAVLQTGLPV ASEERTSGSH LVEDGLANVE ESEDFLSIDS LPSSSFTQPV

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541 PKETIPSMED SDVSLTSSPY LTSSIPFGLD SLTSKVKDQL KVSFPLPDAS MEKELIFDGG
601 LGS6SGQKVD LITWPMSETS SEKSAEPLSK PWLEDDDSL LVDKMDSTDQ
661 ISKHSKYEH DRSTHFPEEE PLSGPAVPF ADTAAESASL TLPKHISEVP GVDDCSVTKA
721 PLILTSVAIS ASTDKSDQAD AILREDMEQI TESSNYEWF SEVSHMKPDM QLTWLILPES
781 ERVWTRTSSL EKLSDILAS TPQADRLWL SVTQSTKLPP TITSTLLEDE VMVGQDISL
841 ELDRIGTDYY QPEQVQEQNG KVGSYVEMST SVHSTEMVSV AWPTEGGDDL SYTQTSGLAV
901 VFFSLRVTNM MFSEDLFNKN SLEYKALEQR FLELLVPYLO SNLTGFQNGLE ILNFRNGSIV
961 VNSRMKMFAN VPPNVNNNAV MILEDFTCTA YNTMNLAIK YSLDVESGDE ANPKCFQACN
1021 EFSECLVNPW SGEAKCRCFP GYLSVEERPC QSLCDLQPDF CLNDGKCDIM PCHGAICRCR
1081 VGENWMYRGK HCEEVSEPV IIGITIASV GLLVIFSAII YFFIRTLQAH HDRSERESP
1141 SGSSRQPDLS MFSANAVKN PVYESHRAG EKYEGRYPQH PFYSSASGDV IGLLSREEIR
1201 QMYESSELSR EEIQRMRVL ELYANDPEFA AFVREQQVEE V
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SEQ ID NO:18 Human IPM 200 cDNA sequence, isoform C

1 AACTTAAGC TTGGAGTTTG GAAGTTTCAA GGATTGGAC ACTCAATTA GGAATCTGTC
61 CTCCTCCAT TCCTTTGGTT TTGGCCCAA TGATTATGTT TCCTCTTTT GGAAGATTT
121 CTCCTGGTAT TTTGATATTT GTCTCTGATG AAGGAGACTT TCCATCATTA ACACGACAAA
181 CCTACTTATC TATAGAGGAG ATCCAAGAAC CCAAGAGTGC AGTTTCTTTT CTCCTGCCTT
241 AAGATCAAC AGACCTTTCT CTAGCTACCA AAAAGAAACA GCCTCTGGAG CGCAGAGAAA
301 CTGAAGACA GTGGTTAATC AGAAGCGGGA GATCTATTCT GTTTCCTAAT GGAGTGAAAA
361 TCTGCCACA TGAAGTGTT GCAGAGCGTG TGGCAATCA TGTGAAGTAT TTTAAGTCC
421 GAGTGTGTC GGAAGCTGTC TGGGAAGCCT TCAGAGCTTT TTGGAGTCSA CTCTCTGGGC
481 GTGAGGAATA CTACTTACTG ATGAATTTGT GTGAGGATGG AGTCACAAGT ATATTTGAAA
541 TGGGCAACAA TTTTGTGAAA TCTGTGGAAC ATAGAAGCTT AATCATGAAG AAACCTGACT
601 ATGCAAGAGA AACTGTAAGC AGCTCTGAAC TGCTTTCTCC AGTCCCTGTT GGTGATACCT
661 CAACATTGGG AGACACTACT CTCAGTGTTT ACATCCACAGA GGTGGACGCC TATGAAGGTG
721 CCTCAGAGAA CAGCTTGGAA AGGCCAGAGG AGAGTATTAG CAATGAAAT GAGAATGTGA
781 TAGAAGAGC CACAAAACCA GCAGGTGAAC AGATTGCAGA ATTCAGTATC CACCTTTTGG
841 GGAAGCAGTA CAGGGAAGAA CTACAGGATT CCTCCAGCTT TCACACCCAG CACCTTGAAG
901 AAGAATTTAT TTCAGAGGTT GAAATGTCAT TTAAGTGGTT ACCAGGCTAC AAGGAAATTC
961 GTGTACTTGA ATTTAGTGTC CCCAAGGAAA ATGACAGTGG CGTAGATTGT TACTATGCAG
1021 TTACCTTCAA TGGTGGGCC ATCAGCAATA CCACCTGGGA CCTCATGAGT CTTCATCCCA
1081 ACAAGGTGGA AAACCATGGC CTTGTGGAAC TTGGATGATA ACCCTACATG GTTTATACAA
1141 TCAAGTAAGT CAGAGATTAT ATTGCTGAGA CATTGCAGCA GAAATTTTGT CTGGGGAAGT
1201 CTCTCTTCAA TCCAGATCTC GATTCCCTGC AGCTTATCAA TGTGAGAGCA GTTTTGCCTC
1261 ACCAACTAGA AGATCTAGTT TGGAAACACC AAGTTTCAAG TCTTCAGGGA AGCCGCTCAT
1321 CTATTCTGTG CTTCARACTG GCTTGCTGTG GGCTTCTGAG GAAAGGACTT CTGATCTCA
1381 CTCTGGTAGA CAGCGATTAG CCAATGTTGA AGAGTCAGAA GATTITTTCTT CTATTGATTC
1441 ATTGCCCTCA AGTTTATTCA CTCACCTGT GCCAAAAGAA ACAATACCAT CCATGGGAAGA
1501 CTCTGTGTGT TCCTTAACAT CTTCACCAT TCTGACCTCT CTTTCTCTGC CAGAGGATC
1561 CTCTTGACC TCCAAAGTCA AAGACCAATT AAAAGTGAGC CCTTCTCTGC CAGAGGATC
1621 CATGGAAGAA GAGTTAATAT TTGACGCTGG TTTAGGTTCA CCGTCTGGG CAAGGTGAGA
1681 TCTGATTACT TGGCCATGGA GTGAGACTTC ATCAGAGAAG AGCCGCTGAC CACTGTCGAA
1741 CGCGTGCTTT GAAGATGAT ATTCACTTTT GCGAGCTGAG ATTTGAAGCA AGAACTAGT
1801 TTTAGTTGAC AAAATGGATT CCACAGACCA AATTAGTAAG CACTCAAAAT ATGAACATGA
1861 TGACAGATCT ATACACTTTC CAGAGGAAGA GCCTCTTAGT GGGCTCTGCT TGCCACTCTT
1921 CGCAGATTAC GACGCTGAAT CTGCGTCTCT AGCCCTCCCC AAGCATATAT CAGAAGTACC
1981 TGGTGTGTGAT GATTACTCAG TTACCAAAAG ACCTCTTATA CTGACATCTG TAGCAATCTC
2041 TGCTCTACT GATAAATCAG ATCAGGCGAGA TGCCATCCTA AGGGAGGATG TGGAGCAAAAT
2101 TACTGAGTCA TCCAACTATG AATGGTTTGA CAGTGAGGTT TCAATTGGTAA AGCCAGATAT
2161 GCAAACTTTG TGCACTATAT TGCCAGAACT AGAGAGAGTT TGGACAAGAA GTTCTCCCT
2221 AGAGAAATTT TGCAGAGACA TATTGGCAAG TACACCACAG AGTGCTGACA GGCTCTGGTT
2281 ATCTGTGAGA CAGTCTACCA AATTGCCTCC AACCACAATC TCCACCCTGAT TAGAGGATGA
2341 AGTAATTATG GGTGTACAGG ATATTTCTGT AGAAGTGGAC CGGATAGGCA CAGATTACTA

2401 TCAGCCTGAG CAAGTCCAAG AGCAAAATGG CAAGGTTGGT AGTTATGTGG AAATGTCAAC
 2461 AAGTGTTCAC TCCACAGAGA TGGTTAGTGT GGCTTGGCCC ACAGAAGGAG GAGATGACTT
 2521 GAGTTATACC CAGACTTCAG GAGCTTTGGT GGTTTTCTTC AGCCTCCGAG TGACTAATAT
 2581 GATGTTTTCA GAAGACTCTGT TTAATAAAAA CTCCTTGGAG TATAAGCCCC TGGAGCAAAAG
 2641 ATTCCTTAGAA TTGCTGGTTC CCTATCTCCA GTCAAATCTC ACGGGGTTCC AGAACTTAGA
 2701 AATCCTCAAC TTCAGAAATG GCAGCATTTG GGTGAACAGT CGAATGAAGT TTGCCAATTC
 2761 TGTCCTCTCT AACGTCAACA ATGCGGTGTA CATGATTCTG GAAGACTTTT GTACCACTGC
 2821 CTACAATACC ATGAACCTGG CTATTGATAA ATACTCTCTT GATGTGGAAT CAGGTGATGA
 2881 AGCCAACCCCT TGCAAGTTTC AGGCCTGTAA TGAATTTTCA GAAGTGCTG GTCAACCCCT
 2941 GGAGTGAGAGA AACAAAAGTG CAGA
 //

SEQ ID NO:19 Human IPM 200 amino acid sequence, isoform C

1 MIMFPLFGKI SLGILIFVLI EGDFFPSLTAQ TYLSIEEIQE PKSAVSFLLP EESTDLSLAT
 61 KKKQPLDRRE TERQWLIRRR RSILFPNGVK ICPDESVAEA VANHVKYFKV RVCQEAVWEA
 121 FRTFWDXLPG REEYHYWMNL CEDGVTSIFE MGTNFSSEVE HRSILMKKLT YAKETVSSSE
 181 LSSPVPVGDV STLGDITLSV PHPEVDAYEG ASESSLERPE ESISNEIENV IEETKPKAGE
 241 QIAEFSIHLL GKQYREELQD SSSFHHQHLE EEFISEVENA FTGLPGYKEI RVLEFRSPKE
 301 NDSGVDVYVA VTFNGEAI SN TTWDLISLHS NKVENHGLVE LDDKPTVVYT ISNFRDYIAE
 361 TLQQNFLLGN SSLNPDPSL QLINVRGVLR HQTEDLVWNT QSSSLQATPS SILCFXLACL
 421 WLLRKGLLDL TW
 //

SEQ ID NO:20 Human IPM 200 cDNA sequence, isoform F

1 TGGAAGTTTC AAGGATTGG AACTCAATT AAGGATTCTG TCCTCTCTCT ATTCCTTTGG
 61 TTTTGGCCCA AATGATTATG TTTCTCTTT TTGGGAAGAT TTCTCTGGGT ATTTTGATAT
 121 TTGTCCTGAT AGAAGGAGAC TTTCCATCAT TAACAGCACA AACCTACTTA TCTATAGAGG
 181 AGATCCAAGC ACTGTGAGGA ATTTGTGTCT GAGGCCGTGA TCATAGGCAT CACTATTGCC
 241 TCCGTGGTGG GACTCTTTGT CATCTTTTCT GCTATCATCT ACTTCTTCAT CAGGACTCTT
 301 CAAGCACACC ATGACAGGAG TGAAGAGAG AGTCCCTTCA GTGGCTCCAG CAGGCAGCCT
 361 GACAGCCTCT CATCTATTGA GAATGCTGTG AAGTACAACC CCGTGTATGA AAGTCACAGG
 421 GCTGGATGTG AGAAGTATGA GGGACCCTAT CCTCAGCATC CCTTCTACAG CTCTGCTAGC
 481 GGAGACGTGA TTGGTGGGCT GAGCAGAGAA GAAATCAGAC AGATGTATGA GAGCAGTAGC
 541 CTTTCCAGAG AGGAAATTCA AGAGAGAATG AGAGTTTGGG AACTGTATGC CAATGATCCT
 601 GAGTTTGCAG CTTTGTGTAG AGAGCAACAA GTGGAAGAGG TTTAACCAA ACTCTGTCTC
 661 TGAAAGTACT TAGAAGCCTG GAGAAGATGG AGATTACTTG TTAATTATGT CATATAATTA
 721 ACCTGGATTT TAAACACTGT TGAAGAAGA GTTTTCTATG AAAAATTAAT ATATAGGCCA
 781 CACTGTTTTT TTTTCAGCTT AAGTTTTCAG AATGTAGTAA GAGATGTATC CATTTTATT
 841 TCTATAAAGA CTGAATGCTG T

SEQ ID NO:21 Human IPM 200 amino acid sequence, isoform F

1 MIMFPLFGKI SLGILIFVLI EGDFFPSLTAQ TYLSIEEIQ L
 //

SEQ ID NO:22 Human IPM 200, regulatory region

1 GAACACTTGT AATACAAAAC AATTCCTATT TACAAGTTT ACTGGAATA CAAATACAGT
 61 AGTTTACAGA GAACTTTCAT GTCTCTTAAT TCTTAAACAC GACCCCTGTA TACAGGTAGA
 121 GATTATCACA TGTAATTTCT TTGGTGAGTA AACCGGCTCA AAGAGCTTAG GTTATTTACC
 181 AAAATCAAAAT ATTAAGTGAT AAAACCAAGA TTTGAGTCCA GGGTTTCTCA ATCTTAAATA

241 CAGGAATCTT TCTAGATTAC TATGATTCTC AGAAGTTTTT TTTAGCTTTT TGGTCAAGGC
301 TGTCAAAAAG AATAATTGCC AACTTAATAT TTGTTACCTA AGAGTTGTCC CTGTTGTCTG
361 ATTGTCAATA TGAAGCTTTT CTTAAGATTA AACCTTTGACT CAGCTAATAA AATTTTCGGC
421 TTTTTTCTCC TACTCATACA ATAAATTTGG CAAGTAAGTT TCCTATAAGC TTACCAAGTAT
481 TTTGCAAAAT CAACATATGCA AATATATTTA ATGGTCATTT AGGTTTATTA GCTTTTATTA
541 AGGCTGAAAA TGTGGTTTAT TTGAGGCTGT ATTGAAAAAA TATACCTTGA CTTTTCCTAA
601 AGCATAAAAA AACATTGAGG GTGATTTAGC TAACACAATT AGTCAAGGAT TCTCAAGGAG
661 AATGTGGTTT AGATCTTTAC AATACACTTT TTTTCAGAGA ATTTTGGCCAG AGATAACATG
721 AAAATAAAAT TAATTTTCATT GCTATTTGAT AGTAAATCCA AGCTTCCACA GGGATCTGCA
781 TGAATTGCTT TCTACTAGT TTAATTTGAT TAAAAAATG TCTAATAATA GAGAAATTTCA
841 TCTGCAGGGA AAATGTTTTT TGGTTAAGA GTTCCTCATG TAGATAAACA CACTGGGCTC
901 CACATTTAAT GGC AAAATTA GCAACAAAGT TATCGCACAG CTATCATTTA TATTAAGTGC
961 TTAATATGTT CCGGGCACTA CTCTAAGCAA AGTGAAGATT GAATTAGTTA ATTAGTTAAT
1021 TTAATCTCTCA CATTAGCTCT ACCATGAGTT TACTATTTCT ATTCCATTTT ATACGAAGG
1081 AAGGAGACAA AGTAAGTGAT TTTTCTATCA AGGAAGGAAA TTTGCAAGAG AATAGTTTCA
1141 TTACAAAAAC TAAATTTGTA CGTAGCTCTG TATTATTGAA ATGGTAGAT ATCTTATGAG
1201 TGGACTTTTT ATGCTTATAC ATCTTAGTCC CTAGGAAAAAC CCAGAACTAA CAGATTTCAG
1261 AAAGTTGGAA AACTCAGTGA ATTATATGTG AAACACATTA TTCTTAGTGG ACTCGTTGTT
1321 AAAGGCAAGG AGAGTGTTAG TAAAGAGCTT AGGTAGATTA GAATAAGAAA ATTTGCTCTC
1381 TCCATCTGCT CTAATTAGCT TATCTCACCA GCTTTTATAG CATGCTGGTT ATTTTCAGAA
1441 AGAAGTGAGA GCTACTTTGA AAGGACAACC ATTTTCTCTT CCGCTAATTT ATATAGTTT
1501 TGAAGTGGTT GTTCATTCTC AAACATAGAC TTTTAAATGT TATTCTTTCT CTAATACCTC
1561 TTGTTATTGG AAGTTTCAAG GATTTTGACA CTCGAATTAG GATTCTGTCC TCTCCTCATT
1621 CCTTTGGTTT TGGCCCAAAAT GATTATGTTT CCTCTTTTTG GGAAGATTTC TCTGGGTATT
1681 TTGATATTGG TCCTGATAGA AGGAGACTTT CCATCAATTA CAGGTATTTA AAAATCTACA
1741 TTTGTTTGTG TCTTTCCATA TCTGTAGTAT ATGTTCTTCA AAAATAGGAT TATTTGATGT
1801 AGATGCTGTG TCAAAATGGA TCAAAATACT TATTAATCTT TGATATGGCT TCAATTTAAC
1861 CGTTTAAAAA TATCTCCCAA TAATTTTGGT TTTCCTCAT TGTATATTTG TGGTTTAAAC
1921 CTCTACTTTA TTTATTTTGT TGAATTTGGA TGTGATTTA CTGTATTTTG CTTGAAATCT
1981 TGAATGAAAG GAGTGGGAGT TAAATGAAAA AAGATGGACT GCCTCACTCC TCTTTTCTT
2041 AGATATGCAT GCCTGCCAT GATTGGGCA CTGGCTTCTC TATCTTAATG TAGCCCCAAGT
2101 GTCAGTTTCT CTTTAGTTGT TACCTTTTGT ACTGTATCTT CATTATCGAA GACTTGTACT
2161 TACTTTCACT CTGTAGCACA AACCTACTTA TCTATAGAGG AGATCAAGAA ACCCAAGAGT
2221 GCAGTTTCTT TTCTCTGCC TGAAGAATCA ACAGACTCTT CTCTAGCTAC ACCAAAGAAA
2281 CAGCCTCTGG ACCGCAGAGA AACTGAAAGA CAGTGGTTAA TCGAAGGGCG GAGATCTATT
2341 CTGTTTCTTA GTGAGTGAA AATCTGCCCA GATGAAAAGT TCGCAGAGGC TGTGGCAAT
2401 CATGTGAAGT ATTTTAAAGT CCGAGGTAAG CGAACATCCA AATCCTTCAG CTCCATAATG
2461 AAATTTCAAAC ATAGTTTAAT CATTTGTTAG GTAACATGTA AAATCAAAAT TTATGATAAT
2521 TTAGACAGGA CTGAGCCAAA ACTACCTTTT TACTGTTAAG AATATAGTGT TAATGGTAAAT
2581 TTCAGAGAAC GTGTTTACATT AAGAGAGGAG GTTTGTTTTT TTTCAGTGC CAGCTTCAAT
2641 AGGCAATAAT ATCATTTAAT AATGACATGC ACTTTGAACC AAAGGAAGAA CGCTTTCATG
2701 ATTTGAGTTT GTAGCTTTTG GTGCGTTATG TAAGAACTT TTTTCACTG AGGGCACTCA
2761 CAATAAGATG TCTTTTCATT ATTTCAACAA CATATTGAGA GAGGAATGTT CTTAAATCTT
2821 TTTAAGCACT TCAAAAAATC CAGTTTATGT TTTGGGCTAC ATTAATTTTA ATTTTACTTT
2881 CTTCATTACA TAAATGCCT AAGTWTACCG ACAAATAAGC TTTTACCAAG NTATACTCAC
2941 CTGCTTGCCCT TTTAATTTAA TAGTTATTAT ATATACAAAT ATAATGTTTC TATATTTTAT
3001 AGTTTAGATA T

SEQ ID NO:23

Mouse IPM 200 cDNA sequence (partial)

1 CCGTGGCAAA CCATGTGAAG TATTTTAAAG CCCGAGTGTG CCAGGAAGCC ATCTGGGAAG
61 CCTTCAGGAC GTTTTTGGAT CGACTTCCTG GGCCTGATGA ATATCGTCAC TGGATGAATT
121 TATGTGAGGA TGGATGCACA AGTGTATTTG AAATGGGCGC CCTTTTAGT CAGTCTGTGG
181 AACATAGAAA CCTAATCATG AAGAACTCGG CTTACACAAG TGAAGCTGAG AGCAGCTCTG
241 GCAAGGATCA GTCCGTGGG CCGTGTGTG CTTTCCAGT GGTATTTGGT GAGACCTCAA
301 CACTGACAGG TGCTGTCTCC AGTGCTTCTC ATCCAGGGTT GGTCTCGGAG AGCAGCGCAG

361	CGTCACCGCA	GGAGAGTATC	AGCAATGAAA	TTGAGAATGT	GACAGAGGAG	CCCACACAAC
421	CAGCTGCTGA	ACAGATTGCG	GAATTACAGCA	TCCAACCTCT	GGGGAAGCGA	TACAGTGAAG
481	AACTGCGGGA	TCCCTCCAGC	GCCCTCTACC	GGCTCCTCGT	GGAGAGTTT	ATTTTCAGAGG
541	TTGAAAAAGC	ATTACACAGG	TTACCTGGCT	ACAAAGGCGAT	CCGTGTCTTG	GAATTCAGGG
601	CCCCGGAGGA	AAATGACAGT	GGGATAGATG	TTCACTATGC	AGTTACTCTC	AATGGCGAAG
661	CCATCAGCAA	TACCACCTGG	GACCTCATAA	GCCTCTCAGC	CACAAAGGTA	GA AAAACCATG
721	GCCTTTGTAGA	GAGGGATGAT	AAACCCACTG	CTGTCTATAC	AATTAGTAA	TTTAGAGATT
781	ATATTCGCTGA	GACGCTGCAC	CAGAACTTTT	TGATGGGAAA	TTCTCTTTTG	AATCCAGATC
841	CAAAGCTTCT	CCAGCTCATC	AATGTGAGAG	GAGTTTGTCT	CCCCCAACAG	GAAGACATAG
901	TTTGGAAAC	CCAAAGTTCA	AGTCTTCAGG	TGACAACATC	CTCTATTTTN	GTGCTTCAGC
961	CTGACTCTGC	TGTGGCTCCT	GAGGGAAGGA	CTTCTGGATC	TTCTATATTA	GAAGTAGGGT
1021	TAGCCAGCAC	TGAAGAATTA	GAAGATACTT	CTATTGTATG	ATTGCTCTTA	AGCCCATATA
1081	TTCAACCTGT	GCCAAAAGAA	ACAGTACCAC	CTATGGAAGA	CTCTGACACG	GCTCTCTTGT
1141	CCACACCACA	TCTGACCTCT	TCTGCTATAG	AGACCTTTAC	TAAAGACATA	GGGACACCTT
1201	CTGGCTTGG	GTCCTTGGCT	TCAAAACATC	CAGACCAGTT	GGAAAGTATC	CGGTGGTTTG
1261	CAGACACACT	TCTGGAAAAA	GACTTCATTT	TTGAAAAGTG	TTCTGGTTGT	GGGTCTGGGA
1321	AAGATGTAGA	TGTGATTGAT	TGGCCATGGA	GTGAGACTTC	ATTAGAGAAG	ACCATAAAC
1381	CACGTGCAAA	GTCATGGTCT	GAAGAACAGG	ATGCACATTT	ACCAACTGAG	GGTAGAGAAA
1441	AATTACATA	AGATGGCAGA	GTAGATTCCA	CAGAACAAT	TATTAATATCA	CTCAACATA
1501	GATATGGAGA	TAGGCCCAT	CATTTTATAG	AGGAAGANTC	CATGTGTAGA	TCTACTATAC
1561	CCATCTTTGT	AGAGTCCGCA	ACTCCACCTA	CATCTCCAAT	CTTTTCAAAA	CACACTTCAG
1621	ATGTACCGA	CATTGATTCT	TACTCACTTA	CCAAACACCC	CTTTCTACCG	GTACTATAG
1681	CAATCCCTGC	TTCCACTAAG	AAAACAGATG	AGGTACTCAA	GGAGATATAG	GTACATACAG
1741	AATCATCCAG	TCACAAGAA	CTTGACAGTG	AGGTTCCAGT	GTCAAGGCCA	GATATGACG
1801	CTGTGTGGAC	CATGTTGCCA	GAATCAGATA	CAGTTTGGAC	AAGAACCTCT	TCCTTAGGGA
1861	AATGTGCCAG	AGACCAATTG	GCAAGTACAC	CAGAGAGCAC	TGACAGACTC	TGGTTGAAAG
1921	CTTCCATGAC	AGAGTCCACT	GAATTGCCCT	CACCAACCCA	CTCCACCCAG	CTAGAGGAGG
1981	AAGTAAATAT	GGCGGTCCAG	GATATTTTAT	TAGAACAATG	CAGGTATAGC	ACAGATTATT
2041	ATCAGTCCGA	GCTAACTGAA	GAACAACATG	GCAAGGCTGA	CGACTGTATG	GAATGTCTTA
2101	CCAGTGTCTA	CTACACAGAG	ATGCCTATTG	TGGCTCTGCC	CACAAAAGGA	GGTGTCTCTA
2161	GTACACCCAG	ACTGCAGGAG	CATTGGTGGT	TTTCTTCAGC	CTCCGCGTGA	CAAAACATG
2221	TGTTTTAGAA	GACTTGTGTT	ACAAAACTC	TTTGAATAT	AAAGCCCTGG	AACAAAGAT
2281	CTTTAGAACT	TGGCTCCCT	ATCTCCAGTC	AAATCTGTCA	GGGTCTCAGA	AGCTAGAAA
2341	TCCTGAGTTT	AGAAACGGCA	GCATTGTGGT	GAACAGCCGA	GTAGAGTTCG	CCGAGTCTG
2401	CCCCTCCTAT	GTCAACAAGG	CCATGTATAG	GATTTCTGGA	GACTTTTGTG	CCACTGCCT
2461	ACCAAACCAT	AACTTGGATA	TCGATAAGTA	CTCCCTGGAC	GTGGAATCAG	GTGATGAGG
2521	CAAACCTTGC	AAGTTTCAGG	CCTGTAATGA	ATTTTCTGAG	TGTTTGGTAA	ATCCATGGA
2581	GTGGAGAAGCA	GAAGTCAAA	GCTACCTTGG	TCTACCTGAGT	GTGGATGAAC	TGCCTTGTCT
2641	AAAGTCTCTGT	GATCTACAGC	CTGACTTCTG	CTTGAACGAT	GGAAAGTGTG	ACATTATGC
2701	CTGGGCAATGA	GCCATTTGTA	GATGCCGGGT	TGTTTCAAA	TGGTGGTATC	GAGGCAAC
2761	ACTGTGAGGAG	TTTGTGCTG	AGCCCTTTGT	CATAGGCATC	ACTATAGCCT	CTGTGGTTA
2821	CGTTTTCTCT	TGTGCTTCTG	CTGTGCTCTT	TTCTCTGTG	AAGATGCTTC	AACTGACAT
2881	ATGTGAGGAGA	GAAAGGCAGA	GGCCACACG	CTCCAGCAGG	CACCTTGACA	GTCTGTCTAT
2941	CTGTTGAAGAT	GCTATGAAGT	ATAACCTGCT	ATATGAGAGC	CACCTGGCTG	GATGTGAAC
3001	TGATAGAGAAA	TCTATAGCC	AACATCCCTT	CTATAGCTCT	GCTAGTGAAG	AGGTGATTG
3061	GTGGTCTGAG	AGAGAAGAAA	TCAGACAGAT	GTATGAAAGT	AGGCACCTTT	CCAAAGAGG
3121	AAATTCAAGAG	AGAAATGAGGA	TTTTGGAACT	CTGTCTAAT	TGCTCTGAGT	TTGACGCTT
3181	TTGTGAGAGAG	CATCAAAATG	AGGAGCTTTA	ACTTAAATGC	CTGATTTCTG	ACACCAATC
3241	AGAAGCTTGA	GAAGATGGAG	AAGGCTTTGT	CTCTCTGCTG	TTAAGCTAAT	CCAGAAGAA
3301	GAGTTGTGATT	TGAAGAATAA	TAAGGAAACA	TGGGACGCAC	TTCTCATTTCC	AACACTGCA
3361	CTCTAATTTTT	TGGAATGGAG	CAAAAAAATA	ATAAGTGATG	TATTTTATTT	TTCTACATTA
3421	AGAGATGTGTC	AAAAAGAAAT	TAAAGTGGTG	TGAACCTCTG	TTTTGTAAAC	TATTTCTAA
3481	AGCAAAACAA	AAAAAGAAAT	CAAAACCAAA	GCTTAAAGCC	AGACCTTTGA	TCTGGGGCT
3541	CGAGTGGCTCT	GACTCTGACT	TTTTGAGAGC	ATCTCTAAGA	ACTATGCCCC	AGGCTTTCT
3601	AGTAAGAACAT	AAAGTGAGAC	TAATGAGTAA	AGCTTAGAAT	GCGACTGTTT	TGTGACATA
3661	CTCGTTAAAGT	CGAATGAGAT	AGAGGAAGCT	TTGAAGTAA	TTTAATATAG	TTTAAACTT
3721	AAACACTCATC	TAAATAAAAA	TTAGGCTTTT	GGAACAGATT	GCTGAGTCAG	GCAATCTTT

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3781 AGGTGCAGTAT ATCTTGTTTA TGTGTGATGC TTGCTTCCTA TCTGTTCTTG AGCTTCTTG
3841 AGCCCATAGAT CAAGACTACA ATGCTCTTAA ATTAGTTATG TCAATATTGT CCACAGTTT
3901 GGTCTCAATT AGGCACCTT AAGAGGAAGC AAATTGAGGA ATTNCTNTTC ATCAGTTTG
3961 GTTTGTGGACA TACCACTGGG CCTTTTCTT GATTATTAAT TGATGTAGAA AGGCCAGC
4021 TCACATATGGT GGTACTATCC TTAGGCAGGG GTTTGGGGAG TTAAGTTGCA AAAGAAAGG
4081 TAAAGCCAGCT ACAAGAAAGC AGCCAATAAG CACTTTCCTT TGTGGTTTCT TCITCAAC
4141 TCCTGTCTTGG CTCTCTCTA TGGTAGACTA TAACCTATAA GCCAAATAAA CTCTTCTT
4201 GGAA
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SEQ ID NO:24 Mouse IPM 200 amino acid sequence (partial)

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LOCUS      MOUSE IPM 200 1069 AA PROT
DEFINITION Mus musculus IPM 200 core protein, lacks NH-terminus
KEYWORDS   -
FEATURES   From To Definition

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1  VANHVKYFKA RVCQEIWEA FRFTWDR LRG RDEYRHWMLN CEDGVTSVFE MGAHFSQSVE
61  HRNLIMKKLA YTRAEASSSC KDQSCGP ELS FPVPIGETST LTGVASSASY PGLASESSAV
121 SPQESISNEI ENVT EEP TQP AAEQIAEFSI QLLGKRYSEE LRDPSSALYR LLVEEFISFV
181 EKAFTGLPGY KGRIVLEFRA PEENDSGIDV HYAVTFNGEA ISNTTWD LIS LHSNKVENHG
241 LVEMDDKPTA VYTISNFRDY IAETLHQNFL MGNSSLNPD P KPLQLINVRG VLLPQTEDIV
301 WNTQSSSLQV TTSIXVLQP DLVPAPEGRT SSGFIELEGL ASTEELEDTS IDGLPSSPLI
361 QVPVKETVPP MEDSDTALLS TPLHTSSAIE DLTGDIPTPS GLESLASNIS DQLEVIPWFF
421 DTSVEKDFIF ESGLGSGSGK DVDVIDWPWS ETSLEKTKP LSKSWSEEDQ ALLPTEGREK
481 LHIDGRVDST EQIESSEHR YGDRPIHFIE EXSHVRSTIP IFVESATPPT SPIFSKHTSD
541 VPDIDSYSLT KPFLPVTIA IPASTKKTDE VLKEDMVHTE SSSHKELDSE VPVSRPDMQP
601 VWTMLPESDT WMTRTSSLGK LSRDRLASTP ESTDRLWLKA SMTQSTELPS TTHSTQLEEE
661 VIMAVQDISL ELDQVGTDYY QSELTEEHQK KADSVYEMST SVHYTEMPIV ALPTKGGVLS
721 HTQTAGALVV FFSRLVTNML FSEDLFNKNS LEYKALEQR F LELLAPYLQS NLSGFQNL EI
781 LSRFNGSIVV NSRVRFESA PPNVNKAMYR ILEDFTCTAY QTNMLDIDKY SLDVSGDEA
841 NPCKFQACNE FSECLVNWPS GEAKCKCPYG YLSVDELPCQ SLCDLPQDFC LNDGKCDIMP
901 GHGAICRCRV GSNWYRGQH CEEFVSEPFV IGTIIASVVS FLLVASAVVF FLVKMLQAQIN
961 VRRERQRP TS SRHPDSLSS VENAMKYNPA YESHLAGCEL YKSYSQHVF YSSASEEIVG
1021 GLSREEIRQM YESSDL SKEE IQERMRIEL YANDPEFAAF VREHQMEEL
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SEQ ID NO:25 Monkey IPM 200 cDNA sequence (partial)

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LOCUS      MONKEY IPM 546 BP SS-DNA SYN 05-OCT-1998
DEFINITION Macaca fascicularis IPM 200 cDNA, 5' end
ACCESSION  -
KEYWORDS   -
FEATURES   From To Definition
ORF        188 546 IPM 200

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1  GAATTCGGCT TGGACAACCA TTTTCTTTC CGCTAATTTA TAATGGTTTT GAAGTGGTTG
61  TTCAATCTCA AACATAGACT TTTAAATGTT AGGCTTTTCC TATAACTTGT TGTATTGGA
121 AGTTTCAAGG ATTTGGAGCG TCAGTTAAGG ATTTTGTCTC CTCTCATTC CTCTGGTTTT
181 GGCCCAAATG ATTTATGTTT CTCTTTTTGG GAAGATTTC CTGGGTATT TGATATTTGT
241 CCTGATAGGA GACTTTCCAT CGTTAACACG ACAAACTAC TTATCTTTAG AGGAGATCCA
301 AGAAGCAACG AGTCAGTTTT CTTTTCTCCT GCCTGAAGAA TCAACAGACC TTCTCTAGC
361 TACCAAAAAG AAACAGCCTC TGGACCTCAG AGAAACTGAA AGACAGTGGT TACTCAGAAG
421 GCAGGAGTCT ATTCTGTTTC CTAATGGAGT AAAAATCTGC CCAGATGAAA GTGTTACAGA
481 GGCTGTGGCA AATCATGTGA AGTATTTTAA AGTCCGAGTG TGTCAGGAAG CTGTCTGGGA
541 AAAGCC

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SEQ ID NO:26 Monkey IPM 200 amino acid sequence (partial)

LOCUS	MONKEY IPM	119 AA	PROT	SYN	16-OCT-1998
DEFINITION	Macaca fascicularis IPM 200 core protein, NH-terminal fragment				
ACCESSION	-				
KEYWORDS	-				
FEATURES					
DOMAIN	82	114	Definition		
			Native NH-terminus		

1 MIMFPLFGKI SLGILIFVLI GDFPSLTAQT YLSLEEQEP KSAVSVLLPE ESTDLSLATK
61 KKQPLDLRET ERQWLLRRRR SILFPNGVKI CPDESVEAV ANHVYKFVVR VCQEAWEK
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SEQ ID NO:27 Human IPM 150 isoform A variant cDNA sequence (3261 bp)

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taaaccaaga aggttatcct caatcatctg gtatcaatat ataattattt ttcctttntg 60
ttacttttta atgagatttg aggttggtct gtgattgtta tcagaattac catgcacaaa 120
agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att 169
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile
1 5 10
ttt ctc caa gtt caa gga act aaa gat atc tcc att aac ata tac cat 217
Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His
15 20 25 30
tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa 265
Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu
35 40 45
agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat 313
Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp
50 55 60
ttg gca aag cat cga aca aaa aga tcc gca ttt ttc cca acg ggg gtt 361
Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val
65 70 75
aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa 409
Lys Val Cys Pro Glu Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln
80 85 90
gct tat tat aga ttg aga gtg tgt cag gaa gca gta tgg gaa gca tat 457
Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr
95 100 105 110
cgg atc ttt ctg gat cgc atc cct gac aca ggg gaa tat cag gac tgg 505
Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp
115 120 125
gtc agc atc tgc cag cag gag acc ttc tgc ctc ttt gac att gga aaa 553
Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
130 135 140
aac ttc agc aat tcc cag gag cac ctg gat ctt ctc cag cag aga ata 601
Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile
145 150 155
aaa cag aga agt ttc cct gac aga aaa gat gaa ata tct gca gag aag 649
Lys Gln Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys
160 165 170
aca ttg gga gag cct ggt gaa acc att gtc att tca aca gat gtt gcc 697
Thr Leu Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala
175 180 185 190
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aac gtc tca ctt ggg cct ttc cct ctc act cct gat gac acc ctc ctc 745
 Asn Val Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu
 195 200 205
 aat gaa att ctc gat aat aca ctc aac gac acc aag atg cct aca aca 793
 Asn Glu Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr
 210 215 220
 gaa aga gaa aca gaa ttc gct gtg ttg gag gag cag agg gtg gag ctc 841
 Glu Arg Glu Thr Glu Phe Ala Val Leu Glu Glu Glu Arg Val Glu Leu
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 agc gtc tct ctg gta aac cag aag ttc aag gca gag ctc gct gac tcc 889
 Ser Val Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser
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 cag tcc cca tat tac cag gag cta gca gga aag tcc cca ctt cag atg 937
 Gln Ser Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met
 255 260 265
 caa aag ata ttt aag aaa ctt cca gga ttc aaa aaa atc cat gtg tta 985
 Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu
 275 280 285
 gga ttt aga cca aag aaa gaa aaa gat ggc tca agc tcc aca gag atg 1033
 Gly Phe Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Thr Glu Met
 290 295 300
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 Gln Leu Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro
 305 310 315
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 Ala Ser Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu
 320 325 330
 gtc tat cat gga acc atg gag gag gac aag caa cca gaa atc tat ctc 1177
 Val Tyr His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu
 335 340 345
 aca gct aca gac ctc aaa agg ctg atc agc aaa gca cta gag gaa gaa 1225
 Thr Ala Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu
 355 360 365
 caa tct ttg gat gtg ggg aca att cag ttc act gat gaa att gct gga 1273
 Gln Ser Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly
 370 375 380
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 Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser
 385 390 395
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 Phe Ala Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro
 400 405 410
 gtt gaa ccc cag ctt gag aca gtg gac gga gca gag cat ggt cta cct 1417
 Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro
 415 420 425
 gac act tct tgg tct cca cct gct atg gcc tct acc tcc ctg tca gaa 1465
 Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu
 435 440 445
 gct cca cct ttc ttt atg gca tca agc atc ttc tot ctg act gat caa 1513
 Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln
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 ggc acc aca gat aca atg gcc act gac cag aca atg cta gta cca ggg 1561
 Gly Thr Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly
 465 470 475
 ctc acc atc ccc acc agt gat tat tct gca atc agc caa ctg gct ctg 1609
 Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu
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Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala	
495 500 505 510	
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Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp	
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act cct gcc cca tct gag gta cca gag ctc agc gaa tat gtt tct gtc	1753
Thr Pro Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val	
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cca gat cat ttc ttg gag gat acc act cct gtc tca gct tta cag tat	1801
Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr	
545 550 555	
atc acc act agt tct atg acc att gcc ccc aag ggc cga gag ctg gta	1849
Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val	
560 565 570	
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Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu	
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ttc aac aag agc tct ctg gag tac cga gct ctg gag caa caa ttc aca	1945
Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr	
595 600 605	
cag ctg ctg gtt cca tat cta cga tcc aat ctt aca gga ttt aag caa	1993
Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln	
610 615 620	
ctt gaa ata ctt aac ttc aga aac ggg agt gtg att gtg aat agc aaa	2041
Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys	
625 630 635	
atg aag ttt gct aag tct gtg ccg tat aac ctc acc aag gct gtg cac	2089
Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His	
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Gly Val Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu	
655 660 665 670	
gaa ata gac agc tac tct ctc aac att gaa cca gct gat caa gca gat	2185
Glu Ile Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp	
675 680 685	
ccc tgc aag ttc ctg gcc tgc ggc gaa ttt gcc caa tgt gta aag aac	2233
Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn	
690 695 700	
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Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser	
705 710 715	
cag ggg agc ctg gac ggt ctg gaa cca ggc ctc tgt ggc ctg gca caa	2329
Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln	
720 725 730	
agg aat gcg agg tcc tcc agg gaa agg gag ctc cat gcg gtt cca gat	2377
Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp	
735 740 745 750	
cac tct gaa aat caa gca tac aaa act agt gtt aaa agt tcc aaa atc	2425
His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile	
755 760 765	
aac aaa ata aca agg taatcagtaa aagaaattct gaattactga ccgtagaata	2480
Asn Lys Ile Thr Arg	
770	
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atgggtcatc aaaatccaga catacagtca acactgagaa tcagcacaca ccatatttca	2660

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t

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SEQ ID NO:28 Human IPM 150 isoform A variant amino acid sequence

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20 25 30
Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr
35 40 45
Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
50 55 60
Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
65 70 75 80
Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
85 90 95
Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile
100 105 110
Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
115 120 125
Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
130 135 140
Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
145 150 155 160
Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
165 170 175
Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val
180 185 190
Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu Asn Glu
195 200 205
Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr Glu Arg
210 215 220
Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu Ser Val
225 230 235 240
Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser Gln Ser
245 250 255
Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met Gln Lys
260 265 270
Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu Gly Phe
275 280 285
Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met Gln Leu
290 295 300
Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro Ala Ser
305 310 315 320
Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu Val Tyr
325 330 335

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His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu Thr Ala
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 Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu Gln Ser
 355 360 365
 Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly Ser Leu
 370 375 380
 Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser Phe Ala
 385 390 395 400
 Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro Val Glu
 405 410 415
 Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro Asp Thr
 420 425 430
 Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu Ala Pro
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 Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln Gly Thr
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 485 490 495
 Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala Gly Gly
 500 505 510
 Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp Thr Pro
 515 520 525
 Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp
 530 535 540
 His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr
 545 550 555 560
 Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val Val Phe
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 580 585 590
 Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr Gln Leu
 595 600 605
 Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln Leu Glu
 610 615 620
 Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys Met Lys
 625 630 635 640
 Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val
 645 650 655
 Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile
 660 665 670
 Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys
 675 680 685
 Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg
 690 695 700
 Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly
 705 710 715 720
 Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln Arg Asn
 725 730 735
 Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp His Ser
 740 745 750
 Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile Asn Lys
 755 760 765
 Ile Thr Arg
 770